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OM protein - protein search, using sw model

Run on: April 2, 2003, 14:27:44 ; Search time 72 Seconds
(without alignments)
198.025 Million cell updates/sec

Title: US-09-875-221b-9

Perfect score: 559
Sequence: 1 DQMQSPSSLSASVGDRTV.....CQGYNIYPLFFGGTKVEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	559	100.0	107	23	AAE19664 Human TNF40-g11 CD
2	559	100.0	214	23	AAE19664 Antibody Fab and m
3	554	99.1	107	23	AAE19665 Human TNF40-g12 CD
4	520	93.0	107	21	AAV56680 Anti-erythropoietin
5	513	91.8	126	17	AAW04387 Chimeric human/mu
6	509	91.1	126	16	AAW04387 Human/murine chime
7	509	91.1	126	16	AAW04387 Human/murine chime
8	509	91.1	126	17	AAW04380 Chimeric human/mu
9	509	91.1	126	17	AAW04395 Chimeric human/mu
10	509	91.1	269	16	AAW04395 Human ONS-W21 anti

11	509	91.1	269	17	AAW04397 Chimeric human/mu
12	506	90.5	126	16	AAW04397 Human/murine chime
13	506	90.5	126	16	AAW04381 Chimeric human/mu
14	505	90.3	126	16	AAW04381 Human/murine chime
15	505	90.3	126	16	AAW04382 Chimeric human/mu
16	504	90.2	126	16	AAW04382 Human/murine chime
17	504	90.2	126	16	AAW04382 Human/murine chime
18	504	90.2	126	16	AAW04382 Human/murine chime
19	504	90.2	126	17	AAW04386 Chimeric human/mu
20	503	90.0	126	16	AAW04386 Human/murine chime
21	502	89.8	126	16	AAW04386 Human/murine chime
22	502	89.8	126	16	AAW04386 Human/murine chime
23	502	89.8	126	16	AAW04383 Chimeric human/mu
24	502	89.8	126	17	AAW04394 Chimeric human/mu
25	502	89.8	126	17	AAW04394 Human/murine chime
26	500	89.4	126	16	AAW04385 Chimeric human/mu
27	500	89.4	126	17	AAW04385 Human/murine chime
28	498	89.1	126	16	AAW04385 Chimeric human/mu
29	498	89.1	126	16	AAW04390 Chimeric human/mu
30	497.5	89.0	109	16	AAW04390 Humanized anti-PR1
31	497	88.9	102	21	AAW04390 Humanized anti-PR1
32	497	88.9	107	22	AAW04390 Humanized anti-PR1
33	497	88.9	107	22	AAW04390 Humanized anti-PR1
34	497	88.9	107	22	AAW04390 Humanized anti-PR1
35	497	88.9	108	21	AAW04390 Humanized anti-PR1
36	497	88.9	109	23	AAW04390 Humanized anti-PR1
37	497	88.9	126	16	AAW04390 Humanized anti-PR1
38	497	88.9	126	17	AAW04388 Chimeric human/mu
39	497	88.9	126	17	AAW04391 Chimeric human/mu
40	494	88.4	126	16	AAW04391 Human/murine chime
41	493	88.2	108	21	AAW04391 Human/murine chime
42	492	88.0	126	16	AAW04391 Human/murine chime
43	491	87.8	108	21	AAW04391 Human/murine chime
44	491	87.8	126	16	AAW04391 Human/murine chime
45	491	87.8	126	17	AAW04389 Chimeric human/mu

ALIGNMENTS

RESULT 1	AAE19664	standard; Protein: 107 AA.
XX	AAE19664	
AC	AAE19664	
XX		
DT	31-MAY-2002	(first entry)
XX		
DE	Human TNF40-g11 CDR grafted variable light chain (VL) protein.	
XX		
KW	Human: tumour necrosis factor 40; TNF40; osteopathic; cardiant; CDR;	
KW	complementarity determining region; rheumatoid; osteo-arthritis; sepsis;	
KW	congestive heart failure; shock; tissue transplant; tuberculosis; AIDS;	
KW	Acquired Immune Deficiency Syndrome; adult respiratory distress syndrome;	
KW	cachexia; allergy; psoriasis; blood coagulation disorder; thyroiditis;	
KW	inflammatory bone disorder; Crohn's disease; autoimmune disease; burn;	
KW	neoplasia therapy; immunomodulator; vulnary; graft rejection.	
XX		
OS	Homo sapiens.	
PN	WO200194585-A1.	
XX		
PD	13-DEC-2001.	
XX		
PF	05-JUN-2001; 2001WO-GB02477.	
XX		
PR	06-JUN-2000; 2000GB-0013810.	
XX		
PA	(CELL-) CELTECH R & D LTD.	
XX		
PI	Atwal DS, Brown DT, Weir ANC, Poplewell AG, Chapman AP, King DJ;	
XX		
DR	WPI; 2002-216732/27.	

DR N-PSDB; AAD31279.

XX New antibody specific for human tumor necrosis factor (TNF)-alpha,
 PT useful for treating TNF-alpha-mediated diseases, e.g. congestive heart
 PT failure, septic or endotoxic shock, cachexia, adult respiratory
 PT distress syndrome -
 XX
 PS Claim 12; Fig 8; 119pp; English.

XX The invention relates to an antibody molecule having specificity for
 CC human tumor necrosis factor-alpha (TNFalpha) comprising a heavy or light
 CC chain. The antibody or the compound comprising the antibody is useful
 CC for treating or manufacturing a medicament for treating a pathology
 CC mediated by TNFalpha, such as rheumatoid or osteo-arthritis. TNFalpha
 CC mediated diseases which can be treated by the antibody include sepsis,
 CC congestive heart failure, septic or endotoxic shock, cachexia, adult
 CC respiratory distress syndrome, acquired immunodeficiency syndrome (AIDS),
 CC allergies, psoriasis, tuberculosis, inflammatory bone disorders, blood
 CC coagulation disorders, burns, rejection episodes following organ or
 CC tissue transplant, Crohn's disease and autoimmune diseases, such as
 CC thyroiditis. The antibodies may also be used to reduce the side effects
 CC associated with TNFalpha generation during neoplasia therapy, to
 CC eliminate or reduce shock-related symptoms associated with the treatment
 CC or prevention of graft rejection by use of an anti-lymphocyte antibody,
 CC for treating multi-organ failure, or in the diagnosis and imaging of
 CC disease states involving elevated levels of TNF alpha. The present
 CC sequence is complementarity determining (CDR) grafted light chain human
 CC tumour necrosis factor (TNF) 40-gL1 protein.

XX Sequence 107 AA:

Query Match 100.0%; Score 559; DB 23; Length 107;
 Best Local Similarity 100.0%; Pred. No. 7.7e-35;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTPSSLSASVGDRTITCKASQNGTNVAMWYQKRGKAPKALISASFLYSGVY 60
 Db 1 DIQMTPSSLSASVGDRTITCKASQNGTNVAMWYQKRGKAPKALISASFLYSGVY 60

QY 61 RFSGSGSGTDFLTITSSLOPEDFATYYCOQYNIYPLTFGQGTKEIK 107
 Db 61 RFSGSGSGTDFLTITSSLOPEDFATYYCOQYNIYPLTFGQGTKEIK 107

RESULT 2
 AAE19696
 ID AAE19696 standard; Protein; 214 AA.

XX AAE19696;
 AC
 XX
 DT 31-MAY-2002 (first entry)
 DE Antibody Fab and modified Fab fragment grafted light chain protein.

XX
 KW Tumour necrosis factor 40; TNF40; osteopathic; cardiant; vulnery; CDR;
 KW complementarity determining region; rheumatoid; osteo-arthritis; sepsis;
 KW congestive heart failure; shock; tissue transplant; tuberculosis; AIDS;
 KW Acquired Immune Deficiency Syndrome; adult respiratory distress syndrome;
 KW cachexia; allergy; psoriasis; blood coagulation disorder; thyroiditis;
 KW inflammatory bone disorder; Crohn's disease; autoimmune disease; burn;
 KW neoplasia therapy; immunomodulator; graft rejection; antibody.

XX Unidentified.
 OS
 XX
 PN WO200194585-A1.
 PD 13-DEC-2001.
 XX
 PF 05-JUN-2001; 2001WO-GB02477.
 XX
 PR 06-JUN-2000; 2000GB-0013810.
 XX
 PA (CELL-) CELTECH R & D LTD.

XX Athwal DS, Brown DT, Weir AMC, Popplewell AG, Chapman AP, King DJ;
 PI WPI; 2002-216732/27.
 DR N-PSDB; AAD31362.

XX New antibody specific for human tumor necrosis factor (TNF)-alpha,
 PT useful for treating TNF-alpha-mediated diseases, e.g. congestive heart
 PT failure, septic or endotoxic shock, cachexia, adult respiratory
 PT distress syndrome -
 XX
 PS Claim 14; Page 113-114; 119pp; English.

XX The invention relates to an antibody molecule having specificity for
 CC human tumor necrosis factor-alpha (TNFalpha) comprising a heavy or light
 CC chain. The antibody or the compound comprising the antibody is useful
 CC for treating or manufacturing a medicament for treating a pathology
 CC mediated by TNFalpha, such as rheumatoid or osteo-arthritis. TNFalpha
 CC mediated diseases which can be treated by the antibody include sepsis,
 CC congestive heart failure, septic or endotoxic shock, cachexia, adult
 CC respiratory distress syndrome, acquired immunodeficiency syndrome (AIDS),
 CC allergies, psoriasis, tuberculosis, inflammatory bone disorders, blood
 CC coagulation disorders, burns, rejection episodes following organ or
 CC tissue transplant, Crohn's disease and autoimmune diseases, such as
 CC thyroiditis. The antibodies may also be used to reduce the side effects
 CC associated with TNFalpha generation during neoplasia therapy, to
 CC eliminate or reduce shock-related symptoms associated with the treatment
 CC or prevention of graft rejection by use of an anti-lymphocyte antibody,
 CC for treating multi-organ failure, or in the diagnosis and imaging of
 CC disease states involving elevated levels of TNF alpha. The present
 CC sequence is antibody Fab and modified Fab fragment grafted light chain
 CC used in the invention.

XX Sequence 214 AA:

Query Match 100.0%; Score 559; DB 23; Length 214;
 Best Local Similarity 100.0%; Pred. No. 1.4e-34;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTPSSLSASVGDRTITCKASQNGTNVAMWYQKRGKAPKALISASFLYSGVY 60
 Db 1 DIQMTPSSLSASVGDRTITCKASQNGTNVAMWYQKRGKAPKALISASFLYSGVY 60

QY 61 RFSGSGSGTDFLTITSSLOPEDFATYYCOQYNIYPLTFGQGTKEIK 107
 Db 61 RFSGSGSGTDFLTITSSLOPEDFATYYCOQYNIYPLTFGQGTKEIK 107

RESULT 3
 AAE19665
 ID AAE19665 standard; Protein; 107 AA.

XX AAE19665;
 AC
 XX
 DT 31-MAY-2002 (first entry)
 DE Human TNF40-gL2 CDR grafted variable light chain (VL) protein.

XX
 KW Human; tumour necrosis factor 40; TNF40; osteopathic; cardiant; CDR;
 KW complementarity determining region; rheumatoid; osteo-arthritis; sepsis;
 KW congestive heart failure; shock; tissue transplant; tuberculosis; AIDS;
 KW Acquired Immune Deficiency Syndrome; adult respiratory distress syndrome;
 KW cachexia; allergy; psoriasis; blood coagulation disorder; thyroiditis;
 KW inflammatory bone disorder; Crohn's disease; autoimmune disease; burn;
 KW neoplasia therapy; immunomodulator; vulnery; graft rejection.

XX Homo sapiens.
 OS
 XX
 PN WO200194585-A1.
 PD 13-DEC-2001.
 XX
 PF 05-JUN-2001; 2001WO-GB02477.

XX 06-JUN-2000; 2000GB-0013810.
 PR (CELL-) CELTECH R & D LTD.
 XX Athwal DS, Brown DT, Weir ANC, Poplewell AG, Chapman AP, King DJ;
 XX WPI: 2002-216732/27.
 DR N-PSDB; AAD31280.
 XX New antibody specific for human tumor necrosis factor (TNF)-alpha,
 PT useful for treating TNF-alpha-mediated diseases, e.g. congestive heart
 PT failure, septic or endotoxemic shock, cachexia, adult respiratory
 PT distress syndrome -
 XX Example 1; Fig 9; 119pp; English.
 PS
 XX The invention relates to an antibody molecule having specificity for
 CC human tumor necrosis factor-alpha (TNFalpha) comprising a heavy or light
 CC chain. The antibody or the compound comprising the antibody is useful
 CC for treating or manufacturing a medicament for treating a pathology
 CC mediated by TNFalpha, such as rheumatoid or osteo-arthritis. TNFalpha
 CC mediated diseases which can be treated by the antibody include sepsis,
 CC congestive heart failure, septic or endotoxemic shock, cachexia, adult
 CC respiratory distress syndrome, acquired immunodeficiency syndrome (AIDS),
 CC allergies, psoriasis, tuberculosis, inflammatory bone disorders, blood
 CC coagulation disorders, burns, rejection episodes following organ or
 CC tissue transplant, Crohn's disease and autoimmune diseases, such as
 CC thyroiditis. The antibodies may also be used to reduce the side effects
 CC associated with TNFalpha generation during neoplasia therapy, to
 CC eliminate or reduce shock-related symptoms associated with the treatment
 CC or prevention of graft rejection by use of an anti-lymphocyte antibody,
 CC for treating multi-organ failure, or in the diagnosis and imaging of
 CC disease states involving elevated levels of TNF alpha. The present
 CC sequence is complementarity determining (CDR) grafted light chain human
 CC tumour necrosis factor (TNF) 40-gL2 protein.
 XX
 SQ Sequence 107 AA;
 Query Match 99.1%; Score 554; DB 23; Length 107;
 Best Local Similarity 99.1%; Pred. No. 1.8e-34;
 Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGRVITTCASQNVGTNVAWYQOKPEKAKALYSASFISGVPY 60
 DB 1 DIQMTQSPSSLSASVGRVITTCASQNVGTNVAWYQOKPEKAKALYSASFISGVPY 60
 QY 61 RFGSGSGGTFTLTISLQPEDFATYYCOQYNIPLTFGGGTKEIK 107
 DB 61 RFGSGSGGTFTLTISLQPEDFATYYCOQYNIPLTFGGGTKEIK 107
 RESULT 4
 AAY56680
 ID AAY56680 standard; protein; 107 AA.
 AC AAY56680;
 XX
 DT 15-FEB-2000 (first entry)
 XX
 DE Anti-erythropoietin receptor Mab 3G9 light chain variable region.
 XX
 KW Complementarity determining region; antibody; immunogenicity;
 KW Old world ape; Old world monkey; antigen-binding affinity.
 XX
 OS Synthetic.
 OS Mus sp.
 OS Pan troglodytes.
 XX
 PN WO955369-A1.
 XX
 PD 04-NOV-1999.

PF 28-APR-1999; 99WO-US09131.
 XX
 PR 28-APR-1998; 98US-0083367.
 XX
 PA (SMIR) SMITHKLINE BEECHAM CORP.
 XX
 PI Taylor AH;
 XX
 DR WPI: 2000-023265/02.
 XX
 XX Antibodies containing donor complementarity determining regions and
 PT non-human primate acceptor frameworks, having reduced immunogenicity in
 PT humans -
 XX
 PS Example 8; Page 114-115; 123pp; English.
 XX
 XX The invention provides an antibody (Ab) comprising donor CDRs
 CC (complementarity determining regions) derived from a non-human antigen-
 CC specific donor antibody, and an acceptor framework from a non-human
 CC primate. The Abs are prepared by grafting CDRs from a non-human antigen-
 CC specific donor antibody onto homologous Old World ape or monkey acceptor
 CC frameworks. The Abs have reduced immunogenicity and are better tolerated
 CC in humans (because of the close similarity between the human and primate
 CC proteins), but retain the full antigen-binding affinity of the donor
 CC antibody.
 XX
 SQ Sequence 107 AA;
 Query Match 93.0%; Score 520; DB 21; Length 107;
 Best Local Similarity 94.4%; Pred. No. 6.2e-32;
 Matches 101; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGRVITTCASQNVGTNVAWYQOKPEKAKALYSASFISGVPY 60
 DB 1 DIQMTQSPSSLSASVGRVITTCASQNVGTNVAWYQOKPEKAKALYSASFISGVPY 60
 QY 61 RFGSGSGGTFTLTISLQPEDFATYYCOQYNIPLTFGGGTKEIK 107
 DB 61 RFGSGSGGTFTLTISLQPEDFATYYCOQYNIPLTFGGGTKEIK 107
 RESULT 5
 AAM04387
 ID AAM04387 standard; protein; 126 AA.
 AC AAM04387;
 XX
 DT 09-DEC-1996 (first entry)
 XX
 DE Chimeric human/murine Mab ONS-M21 fragment HEF-RVL-M21h-g(kappa).
 XX
 KW Murine; human; myeloblastoma; chimeric; monoclonal antibody;
 KW chimera; single stranded Fv region; low human antigenicity;
 KW diagnosis; treatment; cerebral tumour; reshaped.
 XX
 OS Synthetic.
 XX
 FH Key
 FH Peptide
 FT 1..19
 FT /label= sig-peptide
 FT 20..125
 FT /label= mat-peptide
 FT 33..53
 FT /label= CDR_1
 FT 69..75
 FT /label= CDR_2
 FT 108..116
 FT /label= CDR_3
 FT Region
 XX
 XX JP08169900-A.
 XX
 PN 02-JUL-1996.

```
PF 18-NOV-1994; 94JP-0285057.
XX
XX 18-OCT-1994; 94JP-0252166.
PR 19-NOV-1993; 93JP-0291078.
XX
PA (CHUS ) CHUGAI PHARM CO LTD.
XX
XX WPI; 1996-358509/36.
DR N-PSDB; AAT38628.
XX
PT Reshaped anti-human myeloblastoma cell human antibody - has low
PT human antigenicity, and is therefore useful for diagnosis and
PT treatment of cerebral tumours, e.g. myeloblastoma
XX
XX Example 5; Page 30; 45pp; Japanese.
PS
XX The present sequence is a fragment of the chimaeric human/murine
CC monoclonal antibody (Mab) ONS-M21. The Mab was prepd. by
CC combining light and heavy variable region DNA, from a murine
CC anti-human myeloblastoma cell Mab, with human light and heavy
CC constant region sequences, respectively to produce chimaeric
CC human/murine light and heavy chain DNA mols.. A recombinant vector
CC for the expression of the heavy and light chain DNA mols. was
CC prepd., and used to transform a host cell. The host cell was then
CC cultured, and the expression prods. of the heavy and light chain
CC DNA mols. sepd. and connected with a peptide linker to produce a
CC single stranded Fv region. The reshaped Fv region has low human
CC antigenicity, and is therefore expected to be useful as an agent
CC for the diagnosis and treatment of cerebral tumours,
CC e.g. myeloblastoma.
XX
SQ Sequence 126 AA;

Query Match 91.8%; Score 513; DB 17; Length 126;
Best Local Similarity 92.5%; Pred. No. 2.4e-31;
Matches 99; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTYITCKASQNVGNVAMYQOKPGKAPRALYTSASFYSGVPY 60
DB 20 DIQMTQSPSSLSASVGDRTYITCKASQNVGNVAMYQOKPGKAPRLYTSASFYSGVPS 79
QY 61 RFSGSGSGTDFLTITSSLOPEDFATYVCOQYNIYPLTFGSGGKVEIK 107
DB 80 RFSGSGSGTDFLTITSSLOPEDFATYVCOQYNSYPRAFGQGIKVEIK 126

RESULT 6
AAR76680
ID AAR76680 standard; Protein: 126 AA.
XX
AC AAR76680;
XX
XX 17-JAN-1996 (first entry)
DE Human/murine chimeric antibody HEF-RVL-M21p-g kappa.
XX
XX Human; murine; chimeric antibody; HEF-RVL-M21p-g kappa;
KW medulloblastoma; brain tumour; treatment; diagnosis.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1..19
FT Peptide /label= sig-peptide
FT 20..43
FT Peptide /label= FR 1
FT 44..54
FT Peptide /label= CDR 1
FT 55..69
FT Peptide /label= FR 2
FT 70..76
FT Peptide /label= CDR 2
FT 77..108
FT Peptide
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FT FT /label= FR 3
FT FT 109..117
FT FT /label= CDR 3
FT FT Peptide 118..126
FT FT /label= FR 4

XX W09514041-A1.
XX
XX PD 26-MAY-1995.
XX
XX PF 19-OCT-1994; 94WO-JP01763.
XX
XX PR 19-NOV-1993; 93JP-0291078.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX PI Ohmoto T, Sato K, Tsuchiya M;
XX
XX WPI; 1995-200347/26.
DR N-PSDB; AAQ94532.
XX
XX Reconstituted antibody against human medullo:blastoma cells -
PT contains high proportion of human antibody origin and has low
PT antigenicity
XX
XX Claim 24; Pages 90-91; 120pp; Japanese.
PS
XX CC AAQ94532 encodes AAR76680 the human/murine chimeric antibody HEF-
CC RVL-M21p-g kappa. The antibody is reactive with human medullo-
CC blastoma (a brain tumour) cells. The chimeric antibody can be
CC used in the diagnosis and treatment of this disease.
XX
SQ Sequence 126 AA;

Query Match 91.1%; Score 509; DB 16; Length 126;
Best Local Similarity 91.6%; Pred. No. 4.7e-31;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTYITCKASQNVGNVAMYQOKPGKAPRALYTSASFYSGVPY 60
DB 20 DIQMTQSPSSLSASVGDRTYITCKASQNVGNVAMYQOKPGKAPRLYTSASFYSGVPS 79
QY 61 RFSGSGSGTDFLTITSSLOPEDFATYVCOQYNIYPLTFGSGGKVEIK 107
DB 80 RFSGSGSGTDFLTITSSLOPEDFATYVCOQYNSYPRAFGQGIKVEIK 126

RESULT 7
AAR76665
ID AAR76665 standard; Protein: 126 AA.
XX
AC AAR76665;
XX
XX 17-JAN-1996 (first entry)
DE Human/murine chimeric antibody HEF-RVL-M21a-g kappa.
XX
XX Human; murine; chimeric antibody; HEF-RVL-M21a-g kappa;
KW medulloblastoma; brain tumour; treatment; diagnosis.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1..19
FT Peptide /label= sig-peptide
FT 20..43
FT Peptide /label= FR 1
FT 44..54
FT Peptide /label= CDR 1
FT 55..69
FT Peptide /label= FR 2
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FT Peptide /label= CDR 2
FT 77..108
FT Peptide
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FT Peptide 77..108
FT /label= FR 3
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XX WO9514041-A1.
XX
XX 26-MAY-1995.
XX
XX 19-OCT-1994; 94WO-JP01763.
XX
XX 19-NOV-1993; 93JP-0291078.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Ontomo T, Sato K, Tsuchiya M;
XX
XX WPI: 1995-200347/26.
XX
XX N-PSDB: AAQ94499.
XX
XX Reconstituted antibody against human medulloblastoma cells -
XX contains high proportion of human antibody origin and has low
XX antigenicity
XX
XX Claim 33; Page 64; 120pp; Japanese.
XX
XX AAQ94499 encodes AAR7665 the human/murine chimeric antibody HEF-
XX RVL-W21a-g kappa. The antibody is reactive with human medullo-
XX blastoma (a brain tumour) cells. The chimeric antibody can be
XX used in the diagnosis and treatment of this disease.
XX
XX Sequence 126 AA;
XX
XX Query Match 91.1%; Score 509; DB 16; Length 126;
XX Best Local Similarity 91.6%; Pred. No. 4.7e-31;
XX Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 1 DIQMTQSPSSLSASVGRVYTITCKASQNVGTVAMVYQOKPGKAPKALITYSASYSGVPY 60
DB 20 DIQMTQSPSSLSASVGRVYTITCKASQNVGTVAMVYQOKPGKAPKALITYSASYSGVPS 79
OY 61 RFSGSGSTDEFTLTISLQPEDFATYYCOQYNIVPLTFGQGTKEIK 107
DB 80 RFSGSGSTDEFTLTISLQPEDFATYYCOQYNIVPLTFGQGTKEIK 126

RESULT 8
AAW04380
ID AAW04380 standard; Protein: 126 AA.
XX
XX AAW04380;
XX
XX 09-DEC-1996 (first entry)
XX
XX Chimaeric human/murine MAb ONS-W21 fragment HEF-RVL-W21a-g(kappa).
XX
XX Murine: human; myeloblastoma; chimaera; monoclonal antibody;
XX chimaera; single stranded Fv region; low human antigenicity;
XX diagnosis; treatment; cerebral tumour; reshaped.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..19
XX /label= sig_peptide
XX Peptide 20..125
XX /label= mat_peptide
XX Region 33..53
XX /label= CDR_1
XX Region 69..75
XX /label= CDR_2
XX

```

```

FT Region 108..116
FT /label= CDR_3
XX
XX JP08169900-A.
XX
XX 02-JUL-1996.
XX
XX 18-NOV-1994; 94JP-0285057.
XX
XX 18-OCT-1994; 94JP-0252166.
XX
XX 19-NOV-1993; 93JP-0291078.
XX
XX (CHUS ) CHUGAI PHARM CO LTD.
XX
XX WPI: 1996-358509/36.
XX
XX N-PSDB: AAT38613.
XX
XX Reshaped anti-human myeloblastoma cell human antibody - has low
XX human antigenicity, and is therefore useful for diagnosis and
XX treatment of cerebral tumours, e.g. myeloblastoma
XX
XX Example 5; Page 24; 45pp; Japanese.
XX
XX The present sequence is a fragment of the chimaeric human/murine
XX monoclonal antibody (MAb) ONS-W21. The MAb was prepd. by
XX combining light and heavy variable region DNA, from a murine
XX anti-human myeloblastoma cell MAb, with human light and heavy
XX constant region sequences, respectively to produce chimaeric
XX human/murine light and heavy chain DNA mols.. A recombinant vector
XX for the expression of the heavy and light chain DNA mols. was
XX prepd., and used to transform a host cell. The host cell was then
XX cultured, and the expression prods. of the heavy and light chain
XX DNA mols. sepd. and connected with a peptide linker to produce a
XX single stranded Fv region. The reshaped Fv region has low human
XX antigenicity, and is therefore expected to be useful as an agent
XX e.g. myeloblastoma.
XX
XX Sequence 126 AA;
XX
XX Query Match 91.1%; Score 509; DB 17; Length 126;
XX Best Local Similarity 91.6%; Pred. No. 4.7e-31;
XX Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 1 DIQMTQSPSSLSASVGRVYTITCKASQNVGTVAMVYQOKPGKAPKALITYSASYSGVPY 60
DB 20 DIQMTQSPSSLSASVGRVYTITCKASQNVGTVAMVYQOKPGKAPKALITYSASYSGVPS 79
OY 61 RFSGSGSTDEFTLTISLQPEDFATYYCOQYNIVPLTFGQGTKEIK 107
DB 80 RFSGSGSTDEFTLTISLQPEDFATYYCOQYNIVPLTFGQGTKEIK 126

RESULT 9
AAW04395
ID AAW04395 standard; Protein: 126 AA.
XX
XX AAW04395;
XX
XX 09-DEC-1996 (first entry)
XX
XX Chimaeric human/murine MAb ONS-W21 fragment HEF-RVL-W21p-g(kappa).
XX
XX Murine: human; myeloblastoma; chimaera; monoclonal antibody;
XX chimaera; single stranded Fv region; low human antigenicity;
XX diagnosis; treatment; cerebral tumour; reshaped.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..19
XX /label= sig_peptide
XX Peptide 20..125
XX

```

```

FT      Region      /label= mat_peptide
FT      Region      33..53
FT      Region      /label= CDR_1
FT      Region      69..75
FT      Region      /label= CDR_2
FT      Region      108..116
FT      Region      /label= CDR_3
PN      JP08169900-A.
PD      02-JUL-1996.
PF      18-NOV-1994; 94JP-0285057.
PR      18-OCT-1994; 94JP-0252166.
PR      19-NOV-1993; 93JP-0291078.
PA      (CHUS ) CHUGAI PHARM CO LTD.
XX
XX      WPI: 1996-358509/36.
DR      N-PSDB; AAT38646.
XX
XX      Reshaped anti-human myeloblastoma cell human antibody - has low
PT      human antigenicity, and is therefore useful for diagnosis and
PT      treatment of cerebral tumours, e.g. myeloblastoma
XX
PS      Example 5; Page 37; 45pp; Japanese.
XX
XX      The present sequence is a fragment of the chimaeric human/murine
CC      monoclonal antibody (Mab) ONS-M21. The Mab was prepd. by
CC      combining light and heavy variable region DNA, from a murine
CC      anti-human myeloblastoma cell Mab, with human light and heavy
CC      constant region sequences, respectively to produce chimaeric
CC      human/murine light and heavy chain DNA mols.. A recombinant vector
CC      for the expression of the heavy and light chain DNA mols. was
CC      prepd., and used to transform a host cell. The host cell was then
CC      cultured, and the expression prods. of the heavy and light chain
CC      DNA mols. sepd. and connected with a peptide linker to produce a
CC      single stranded Fv region. The reshaped Fv region has low human
CC      antigenicity, and is therefore expected to be useful as an agent
CC      for the diagnosis and treatment of cerebral tumours,
CC      e.g. myeloblastoma.
XX
SQ      Sequence 126 AA:

Query Match      91.1%; Score 509; DB 17; Length 126;
Best Local Similarity 91.6%; Pred. No. 4.7e-31;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY      1 DIQMTQSPSSLSASVDRTYITCKASQNGTNVAMWQOKPGKAPKALISASFLYSGVPY 60
      |||||||
DB      20 DIQMTQSPSSLSASVDRTYITCKASQNGTNVAMWQOKPGKAPKALISASFLYSGVPS 79
QY      61 RPSGSGSGTDFLTLSLQPEDFATYYCOQYNITPLTFGQGTVEIK 107
      |||||||
DB      80 RPSGSGSGTDFLTLSLQPEDATYYCOQYNSYPRAFGQGTVEIK 126

RESULT 10
AAR76682
ID      AAR76682 standard; Protein; 269 AA.
XX
AC      AAR76682;
XX
DT      18-JAN-1996 (first entry)
XX
DE      Human ONS-M21 antibody Fv fragment.
XX
XX      Plasmid pSCFV7-hm21; human; ONS-M21 antibody; chimeric protein;
KM      medulloblastoma; brain tumour; treatment; diagnosis; Fv fragment.
XX
OS      Homo sapiens.
XX

```

```

FH      Key      Location/Qualifiers
FH      Peptide  1..22
FT      Region  23..139
FT      Region  /note= "heavy variable region"
FT      Region  140..154
FT      Region  /note= "linker"
FT      Region  155..269
FT      Region  /note= "light variable region"
FT      Region  262..269
FT      Region  /note= "FLAG"
PN      WO9514041-A1.
PD      26-MAY-1995.
PF      19-OCT-1994; 94WO-JP01763.
PR      19-NOV-1993; 93JP-0291078.
PA      (CHUS ) CHUGAI SEIYAKU KK.
XX
XX      Ohtomo T, Sato K, Tsuchiya M;
PI      WPI: 1995-200347/26.
DR      N-PSDB; AAQ94548.
XX
XX      Reconstituted antibody against human medullo:blastoma cells -
PT      contains high proportion of human antibody origin and has low
PT      antigenicity
XX
PS      Claim 35; Pages 98-99; 120pp; Japanese.
XX
XX      AAQ94548 is the plasmid pSCFV7-hm21, which encodes AAR76682 the
CC      human antibody ONS-M21 Fv fragment. The plasmid was used in the
CC      construction of an expression vector, contg. cDNA encoding a
CC      human/murine chimeric antibody, reactive with human medullo-
CC      blastoma (a brain tumour) cells. The chimeric antibody can be
CC      used in the diagnosis and treatment of this disease.
XX
SQ      Sequence 269 AA:

Query Match      91.1%; Score 509; DB 16; Length 269;
Best Local Similarity 91.6%; Pred. No. 9.3e-31;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY      1 DIQMTQSPSSLSASVDRTYITCKASQNGTNVAMWQOKPGKAPKALISASFLYSGVPY 60
      |||||||
DB      155 DIQMTQSPSSLSASVDRTYITCKASQNGTNVAMWQOKPGKAPKALISASFLYSGVPS 214
QY      61 RPSGSGSGTDFLTLSLQPEDFATYYCOQYNITPLTFGQGTVEIK 107
      |||||||
DB      215 RPSGSGSGTDFLTLSLQPEDATYYCOQYNSYPRAFGQGTVEIK 261

RESULT 11
AAW04397
ID      AAW04397 standard; Protein; 269 AA.
XX
AC      AAW04397;
XX
DT      09-DEC-1996 (first entry)
XX
DE      Chimaeric human/murine Mab ONS-M21 scFv fragment.
XX
XX      Murine; human; myeloblastoma; chimaera; monoclonal antibody;
KM      chimeric; single stranded Fv region; low human antigenicity;
KM      diagnosis; treatment; cerebral tumour; reshaped.
XX
OS      Synthetic.
XX
XX      Key      Location/Qualifiers
FH      Peptide  1..22

```

```

FT      Region      /label= sig_peptide
FT      23..139
FT      /note= "heavy variable region"
FT      Peptide      140..154
FT      /label= linker
FT      Region      155..261
FT      /note= "light variable region"
FT      Peptide      262..269
FT      /label= FLAG
XX      JP08169900-A.
XX      02-JUL-1996.
XX      18-NOV-1994; 94JP-0285057.
XX      18-OCT-1994; 94JP-0252166.
XX      19-NOV-1993; 93JP-0291078.
XX      (CHUS ) CHUGAI PHARM CO LTD.
XX      WPI; 1996-358509/36.
XX      N-PSDB; AAT3866Z.
XX      Reshaped anti-human myeloblastoma cell human antibody - has low
XX      human antigenicity, and is therefore useful for diagnosis and
XX      treatment of cerebral tumours, e.g. myeloblastoma
XX      Example 6; Pages 40-41; 45pp; Japanese.
XX      PS
XX      CC The present sequence is a scfv fragment from the chimaeric
XX      CC human/murine monoclonal antibody (Mab) ONS-M21. The Mab was
XX      CC prep'd. by combining light and heavy variable region DNA from a
XX      CC murine anti-human myeloblastoma cell Mab, with human light and
XX      CC heavy constant region sequences, respectively to produce chimeric
XX      CC human/murine light and heavy chain DNA mols. A recombinant vector
XX      CC for the expression of the heavy and light chain DNA mols. was
XX      CC prep'd., and used to transform a host cell. The host cell was then
XX      CC cultured, and the expression prods. of the heavy and light chain
XX      CC DNA mols. sepd. and connected with a peptide linker to produce a
XX      CC single stranded Fv region. The reshaped Fv region has low human
XX      CC antigenicity, and is therefore expected to be useful as an agent
XX      CC for the diagnosis and treatment of cerebral tumours,
XX      CC e.g. myeloblastoma.
XX      CC
SQ      Sequence 269 AA:
Query Match 91.1%; Score 509; DB 17; Length 269;
Best Local Similarity 91.6%; Pred. No. 9.3e-31;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
OY      1 DIQMTQSPSSISASVGRVITTCASQNVGTVAMVYQOKPGKAPKALYLSFLYSGVPY 60
DB      155 DIQMTQSPSSISASVGRVITTCASQNVGTVAMVYQOKPGKAPKALYLSFLYSGVPS 214
OY      61 RFSGSGGTDFLTITSSLOPEDFATYVCOQYNYPLTFGGGTKEIK 107
DB      215 RFSGSGGTDFLTITSSLOPEDATYVCOQYNSYPRAFGGGTKEIK 261

```

RESULT 12
AAR76666
ID AAR76666 standard; Protein; 126 AA.

XX AAR76666;
XX
XX 17-JAN-1996 (first entry)
XX
DE Human/murine chimeric antibody HEF-RVL-M21b-g kappa.
XX
XX Human; murine; chimeric antibody; HEF-RVL-M21b-g kappa;
KW medulloblastoma; brain tumour; treatment; diagnosis;
XX

```

OS      Homo sapiens.
XX      Key      Location/Qualifiers
XX      Peptide      1..19
XX      /label= sig_peptide
XX      Peptide      20..43
XX      /label= FR 1
XX      Peptide      44..54
XX      /label= CDR 1
XX      Peptide      55..69
XX      /label= FR 2
XX      Peptide      70..76
XX      /label= CDR 2
XX      Peptide      77..108
XX      /label= FR 3
XX      Peptide      109..117
XX      /label= CDR 3
XX      Peptide      118..126
XX      /label= FR 4
XX      WO9514041-A1.
XX      26-MAY-1995.
XX      19-OCT-1994; 94WO-JP01763.
XX      19-NOV-1993; 93JP-0291078.
XX      (CHUS ) CHUGAI SEIYAKU KK.
XX      Ontomo T, Sato K, Tsuchiya M;
XX      WPI; 1995-200347/26.
XX      Reconstituted antibody against human medullo:blastoma cells -
XX      PT contains high proportion of human antibody origin and has low
XX      PT antigenicity
XX      PS Claim 33; Page 66; 120pp; Japanese.
XX      CC AA094502 encodes AAR76666 the human/murine chimeric antibody HEF-
XX      CC RVL-M21b-g kappa. The antibody is reactive with human medullo-
XX      CC blastoma (a brain tumour) cells. The chimeric antibody can be
XX      CC used in the diagnosis and treatment of this disease.
XX      CC
SQ      Sequence 126 AA:
Query Match 90.5%; Score 506; DB 16; Length 126;
Best Local Similarity 90.7%; Pred. No. 7.9e-31;
Matches 97; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
OY      1 DIQMTQSPSSISASVGRVITTCASQNVGTVAMVYQOKPGKAPKALYLSFLYSGVPY 60
DB      20 DIQMTQSPSSISASVGRVITTCASQNVGTVAMVYQOKPGKAPKALYLSFLYSGVPS 79
OY      61 RFSGSGGTDFLTITSSLOPEDFATYVCOQYNYPLTFGGGTKEIK 107
DB      80 RFSGSGGTDFLTITSSLOPEDATYVCOQYNSYPRAFGGGTKEIK 126

```

RESULT 13
AAW04381
ID AAW04381 standard; Protein; 126 AA.

XX AAW04381;
XX
XX 09-DEC-1996 (first entry)
XX
DE Chimaeric human/murine Mab ONS-M21 fragment HEF-RVL-M21b-g(kappa).
XX
XX Murine; human; myeloblastoma; chimaera; monoclonal antibody;
KW chimaera; single stranded Fv region; low human antigenicity;
diagnosis; treatment; cerebral tumour; reshaped.
XX

```

XX OS Synthetic.
XX Key Location/Qualifiers
FH Peptide 1..19
FT Peptide /label= sig_peptide
FT Peptide 20..125
FT Peptide /label= mat_peptide
FT Region 33..53
FT Region /label= CDR_1
FT Region 69..75
FT Region /label= CDR_2
FT Region 108..116
FT Region /label= CDR_3
PN JP08169900-A.
XX 02-JUL-1996.
XX 18-NOV-1994: 94JP-0285057.
XX 18-OCT-1994: 94JP-0252166.
XX 19-NOV-1993: 93JP-0291078.
XX (CHUS ) CHUGAI PHARM CO LTD.
XX WPI: 1996-358509/36.
XX N-PSDB: AAT38616.
XX
PT Reshaped anti-human myeloblastoma cell human antibody - has low
PT human antigenicity, and is therefore useful for diagnosis and
PT treatment of cerebral tumours, e.g. myeloblastoma
XX
XX Example 5; Page 25; 45pp; Japanese.
XX
CC The present sequence is a fragment of the chimeric human/murine
CC monoclonal antibody (Mab) OMS-M21. The Mab was prepd. by
CC combining light and heavy variable region DNA, from a murine
CC anti-human myeloblastoma cell Mab, with human light and heavy
CC constant region sequences, respectively to produce chimeric
CC human/murine light and heavy chain DNA mols.. A recombinant vector
CC for the expression of the heavy and light chain DNA mols. was
CC prepd., and used to transform a host cell. The host cell was then
CC cultured, and the expression prods. of the heavy and light chain
CC DNA mols. sep'd. and connected with a peptide linker to produce a
CC single stranded Fv region. The reshaped Fv region has low human
CC antigenicity, and is therefore expected to be useful as an agent
CC for the diagnosis and treatment of cerebral tumours,
CC e.g. myeloblastoma.
XX
SQ Sequence 126 AA:

```

```

Query Match 90.5%; Score 506; DB 17; Length 126;
Best Local Similarity 90.7%; Pred. No. 7.9e-31;
Matches 97; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

```

RESULT 14

```

AA076667
ID AAR76667 standard; Protein; 126 AA.
XX
AC AAR76667;
XX
DT 17-JAN-1996 (first entry)
XX

```

```

DE Human/murine chimeric antibody HEF-RVL-M21c-g kappa.
XX
XX Human; murine; chimeric antibody; HEF-RVL-M21c-g kappa;
XX medulloblastoma; brain tumour; treatment; diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..19
FT Peptide /label= sig_peptide
FT Peptide 20..43
FT Peptide /label= FR 1
FT Peptide 44..54
FT Peptide /label= CDR 1
FT Peptide 55..69
FT Peptide /label= FR 2
FT Peptide 70..76
FT Peptide /label= CDR 2
FT Peptide 77..108
FT Peptide /label= FR 3
FT Peptide 109..117
FT Peptide /label= CDR 3
FT Peptide 118..126
FT Peptide /label= FR 4
PN WO9514041-A1.
XX 26-MAY-1995.
XX
XX 19-OCT-1994: 94WO-JP01763.
XX 19-NOV-1993: 93JP-0291078.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Ohtomo T, Sato K, Tsuchiya M;
XX WPI: 1995-200347/26.
XX N-PSDB: AA094505.
XX
PT Reconstituted antibody against human medullo-blastoma cells -
PT contains high proportion of human antibody origin and has low
PT antigenicity
XX
XX Claim 33; Page 68; 120pp; Japanese.
XX
XX AA094505 encodes AAR76667 the human/murine chimeric antibody HEF-
XX RVL-M21c-g kappa. The antibody is reactive with human medullo-
XX blastoma (a brain tumour) cells. The chimeric antibody can be
XX used in the diagnosis and treatment of this disease.
XX
SQ Sequence 126 AA:

```

```

Query Match 90.3%; Score 505; DB 16; Length 126;
Best Local Similarity 90.7%; Pred. No. 9.4e-31;
Matches 97; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

```

RESULT 15

```

AAW04382
ID AAW04382 standard; Protein; 126 AA.
XX
AC AAW04382;
XX
DT 09-DEC-1996 (first entry)
XX

```


XX Chimaeric human/murine MAb ONS-M21 fragment HEF-RVL-M21c-g(kappa).

DE Murine; human; myeloblastoma; chimaera; monoclonal antibody;
 XX chimaera; single stranded Fv region; low human antigenicity;
 KW diagnosis; treatment; cerebral tumour; reshaped.
 KW
 XX
 OS Synthetic.

XX	Key	Location/Qualifiers
XX	Peptide	1..19
XX	Peptide	/label= sig_peptide
XX	Peptide	20..125
XX	Peptide	/label= mat_peptide
XX	Region	33..53
XX	Region	/label= CDR_1
XX	Region	69..75
XX	Region	/label= CDR_2
XX	Region	108..116
XX	Region	/label= CDR_3

XX JP08169900-A.

XX 02-JUL-1996.

XX 18-NOV-1994; 94JP-0285057.

XX 18-OCT-1994; 94JP-0252166.

XX 19-NOV-1993; 93JP-0291078.

XX (CHUS) CHUGAI PHARM CO LTD.

XX WPI: 1996-358509/36.

XX N-PSDB: MAT38619.

XX Reshaped anti-human myeloblastoma cell human antibody - has low
 PT human antigenicity, and is therefore useful for diagnosis and
 PT treatment of cerebral tumours, e.g. myeloblastoma

XX Example 5; Page 26; 45pp; Japanese.

XX The present sequence is a fragment of the chimaeric human/murine
 CC monoclonal antibody (Mab) ONS-M21. The Mab was prepd. by
 CC combining light and heavy variable region DNA, from a murine
 CC anti-human myeloblastoma cell Mab, with human light and heavy
 CC constant region sequences, respectively to produce chimaeric
 CC human/murine light and heavy chain DNA mols.. A recombinant vector
 CC for the expression of the heavy and light chain DNA mols. was
 CC prepd., and used to transform a host cell. The host cell was then
 CC cultured, and the expression prods. of the heavy and light chain
 CC DNA mols. sepd. and connected with a peptide linker to produce a
 CC single stranded Fv region. The reshaped Fv region has low human
 CC antigenicity, and is therefore expected to be useful as an agent
 CC for the diagnosis and treatment of cerebral tumours,
 CC e.g. myeloblastoma.

XX Sequence 126 AA;

Query Match 90.3%; Score 505; DB 17; Length 126;

Best Local Similarity 90.7%; Pred. No. 9.4e-31;

Matches 97; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy	1	DIQMTPSSSSASVGDRTYTCRKSQNVGVNVMYQKPKAKPKALISASFLYSGVPY	60
Db	20	DIQMTPSSSSASVGDRTYTCRKSQNVGVNVMYQKPKAKPKALISASFLYSGVPS	79
Qy	61	RFGSGSGTDFLTITISLOPEDFATYCCQYNIYPLTFGQGTKEIK	107
Db	80	RFGSGSGTDFLTITISLOPEDFATYCCQYNIYPLTFGQGTKEIK	126

Search completed: April 2, 2003, 14:37:06
 Job time : 73 secs

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 2, 2003, 14:35:54 ; Search time 28 Seconds
(without alignments)
112.438 Million cell updates/sec

Title: US-09-875-221B-9
Perfect score: 559
Sequence: 1 DIQMTQSPSSLSASVGRVT.....COQYNIVPLRFGGGRKVEIK 107

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

- 1: Issued Patents_AA:*
- 2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	513	91.8	126	4	US-08-646-265A-65
2	509	91.1	107	4	US-08-646-265A-130
3	509	91.1	126	4	US-08-646-265A-43
4	509	91.1	126	4	US-08-646-265A-91
5	509	91.1	269	4	US-08-646-265A-109
6	506	90.5	126	4	US-08-646-265A-47
7	505	90.3	126	4	US-08-646-265A-51
8	504	90.2	126	4	US-08-646-265A-57
9	504	90.2	126	4	US-08-646-265A-63
10	502	89.8	107	4	US-08-646-265A-131
11	502	89.8	126	4	US-08-646-265A-53
12	502	89.8	126	4	US-08-646-265A-85
13	502	89.8	126	4	US-08-646-265A-87
14	500	89.4	126	4	US-08-646-265A-75
15	498	89.1	126	4	US-08-646-265A-75
16	497.5	89.0	109	2	US-08-602-725-30
17	497	88.9	126	4	US-08-646-265A-69
18	497	88.9	126	4	US-08-646-265A-77
19	491	87.8	126	4	US-08-646-265A-73
20	490	87.7	126	1	US-08-202-047-13
21	490	87.7	126	1	US-08-202-047-15
22	490	87.7	126	3	US-08-964-690-13
23	490	87.7	126	3	US-08-964-690-15
24	486	86.9	126	1	US-08-202-047-17
25	486	86.9	126	1	US-08-202-047-19
26	486	86.9	126	3	US-08-964-690-17
27	486	86.9	126	3	US-08-964-690-19

28	484	86.6	126	4	US-08-646-265A-81	Sequence 81, Appl
29	481	86.0	107	2	US-07-934-373C-41	Sequence 41, Appl
30	481	86.0	107	3	US-08-437-642B-41	Sequence 41, Appl
31	481	86.0	214	4	US-09-679-397-1	Sequence 1, Appl
32	481	86.0	214	4	US-09-680-148-1	Sequence 1, Appl
33	481	86.0	237	2	US-08-463-587A-25	Sequence 25, Appl
34	481	86.0	237	2	US-08-463-667A-3	Sequence 3, Appl
35	481	86.0	237	3	US-08-923-854-25	Sequence 25, Appl
36	481	86.0	237	5	PCT-US91-09133-26	Sequence 26, Appl
37	477	85.3	109	2	US-07-934-373C-3	Sequence 3, Appl
38	477	85.3	109	2	US-08-437-642B-3	Sequence 3, Appl
39	477	85.3	109	4	US-08-146-206C-3	Sequence 3, Appl
40	477	85.3	109	5	PCT-US93-07832-3	Sequence 3, Appl
41	476	85.2	108	3	US-08-974-899-2	Sequence 2, Appl
42	474	84.8	107	2	US-07-934-373C-18	Sequence 18, Appl
43	474	84.8	107	2	US-07-934-373C-43	Sequence 43, Appl
44	474	84.8	107	3	US-08-437-642B-18	Sequence 18, Appl
45	474	84.8	107	3	US-08-437-642B-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-08-646-265A-65
Sequence 65, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshihiko
APPLICANT: SATO, Koh
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-265A-65
Query Match 91.8%; Score 513; DB 4; Length 126;

NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646, 265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-265A-91

Query Match 91.1%; Score 509; DB 4; Length 126;
Best Local Similarity 91.6%; Pred. No. 1.2e-40;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Oy 1 DIOMTQSPSSLSASVGDRTITCKASQNGTVAMVYQKPGKAPRLIYSASFISGVY 60
Db 20 DIOMTQSPSSLSASVGDRTITCKASQNGTVAMVYQKPGKAPRLIYSASFISGVPS 79

Oy 61 RFGSGSGTDFLTITSLQPEDFATYCCQYNIYPLTFGQGTKEIK 107
Db 80 RFGSGSGTDFLTITSLQPEDIATYCCQYNSYRPFQGTKEIK 126

RESULT 5
US-08-646-265A-109
Sequence 109, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshiniko
APPLICANT: SATO, Koh
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646, 265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-265A-109

Query Match 91.1%; Score 509; DB 4; Length 269;
Best Local Similarity 91.6%; Pred. No. 2.8e-40;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Oy 1 DIOMTQSPSSLSASVGDRTITCKASQNGTVAMVYQKPGKAPRLIYSASFISGVY 60
Db 155 DIOMTQSPSSLSASVGDRTITCKASQNGTVAMVYQKPGKAPRLIYSASFISGVPS 214

Oy 61 RFGSGSGTDFLTITSLQPEDFATYCCQYNIYPLTFGQGTKEIK 107
Db 215 RFGSGSGTDFLTITSLQPEDIATYCCQYNSYRPFQGTKEIK 261

RESULT 6
US-08-646-265A-47
Sequence 47, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshiniko
APPLICANT: SATO, Koh
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646, 265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078

FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-265A-47

Query Match
Best Local Similarity 90.5%; Score 506; DB 4; Length 126;
Matches 97; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDRTYITCKASQNGTNAVYQQRKPKAKLIYSASFYSGVPY 60
DB 20 DIQMTQSPSSLSASVDRTYITCKASQNGTNAVYQQRKPKAKLIYSASFYSGVPS 79

QY 61 RFSGSSGTDFTLTISLSLOPEDPATYCCOQYNLYPLTFGGGTVEIK 107
DB 80 RFSGSSGTDFTLTISLSLOPEDPATYCCOQYNLYPLTFGGGTVEIK 126

RESULT 7
US-08-646-265A-51
Sequence 51, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshiniko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:

LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-265A-51

Query Match
Best Local Similarity 90.3%; Score 505; DB 4; Length 126;
Matches 97; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDRTYITCKASQNGTNAVYQQRKPKAKLIYSASFYSGVPY 60
DB 20 DIQMTQSPSSLSASVDRTYITCKASQNGTNAVYQQRKPKAKLIYSASFYSGVPS 79

QY 61 RFSGSSGTDFTLTISLSLOPEDPATYCCOQYNLYPLTFGGGTVEIK 107
DB 80 RFSGSSGTDFTLTISLSLOPEDPATYCCOQYNLYPLTFGGGTVEIK 126

RESULT 8
US-08-646-265A-57
Sequence 57, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshiniko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-265A-57

Query Match
Best Local Similarity 90.2%; Score 504; DB 4; Length 126;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDRTYITCKASQNGTNAVYQQRKPKAKLIYSASFYSGVPY 60

Db 20 DIQMTQSPSSLSASVGDVNTICKASQNVGTNAVYQOKPGKAPRLILYSASFLYSVGP 79
Qy 61 RFSGSGSTDFLTITSSLOPEDFATYYCOQYNIYPLTFGQGTVEIK 107
Db 80 RFSGSGSTDFLTITSSLOPEDFATYYCOQYNSYPRAFGQGTVEIK 126

RESULT 9

US-08-646-265A-63
; Sequence 63, Application US/08646265A
; Patent No. 6214973
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshihiko
; APPLICANT: SATO, Koh
; APPLICANT: TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,265A
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/01763
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-291078
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEFAX: 904136
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-646-265A-63

Query Match 90.2%; Score 504; DB 4; Length 126;
Best Local Similarity 89.7%; Pred. No. 3.6e-40;
Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDVNTICKASQNVGTNAVYQOKPGKAPRLILYSASFLYSVGP 60
Db 20 DIQMTQSPSSLSASVGDVNTICKASQNVGTNAVYQOKPGKAPRLILYSASFLYSVGP 79
Qy 61 RFSGSGSTDFLTITSSLOPEDFATYYCOQYNIYPLTFGQGTVEIK 107
Db 80 RFSGSGSTDFLTITSSLOPEDFATYYCOQYNSYPRAFGQGTVEIK 126

RESULT 10
US-08-646-265A-131
; Sequence 131, Application US/08646265A

Patent No. 6214973
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshihiko
; APPLICANT: SATO, Koh
; APPLICANT: TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,265A
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/01763
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-291078
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEFAX: 904136
; INFORMATION FOR SEQ ID NO: 131:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-646-265A-131

Query Match 89.8%; Score 502; DB 4; Length 107;
Best Local Similarity 89.7%; Pred. No. 4.7e-40;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDVNTICKASQNVGTNAVYQOKPGKAPRLILYSASFLYSVGP 60
Db 1 DIQMTQSPSSLSASVGDVNTICKASQNVGTNAVYQOKPGKAPRLILYSASFLYSVGP 60
Qy 61 RFSGSGSTDFLTITSSLOPEDFATYYCOQYNIYPLTFGQGTVEIK 107
Db 61 RFSGSGSTDFLTITSSLOPEDFATYYCOQYNSYPRAFGQGTVEIK 107

RESULT 11
US-08-646-265A-53
; Sequence 53, Application US/08646265A
; Patent No. 6214973
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshihiko
; APPLICANT: SATO, Koh
; APPLICANT: TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500

CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/011763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-265A-53

Query Match 89.8%; Score 502; DB 4; Length 126;
Best Local Similarity 89.7%; Pred. No. 5.6e-40;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTYITCKASQNYGTNVAMYOQKPGKAPKALISASFLYSGVPY 60
|||
DB 20 DIOMTQSPSSLSASVGDRTYITCKASQNYGTNVAMYOQKPGKAPKALISASFLYSGVPS 79
|||

QY 61 RRSQSGSGTDFLTITSSLOPEDFATYYCOQYNIYPLTFEGQTKVEIK 107
|||||
DB 80 RRSQSGSGTDFLTITSSLOPEDFATYYCOQYNSYPRAFGQTKVEIK 126
|||||

RESULT 12
US-08-646-265A-85
Sequence 85, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshihiko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A

FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/011763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-265A-85

Query Match 89.8%; Score 502; DB 4; Length 126;
Best Local Similarity 89.7%; Pred. No. 5.6e-40;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTYITCKASQNYGTNVAMYOQKPGKAPKALISASFLYSGVPY 60
|||
DB 20 DIOMTQSPSSLSASVGDRTYITCKASQNYGTNVAMYOQKPGKAPKALISASFLYSGVPS 79
|||

QY 61 RRSQSGSGTDFLTITSSLOPEDFATYYCOQYNIYPLTFEGQTKVEIK 107
|||||
DB 80 RRSQSGSGTDFLTITSSLOPEDFATYYCOQYNSYPRAFGQTKVEIK 126
|||||

RESULT 13
US-08-646-265A-87
Sequence 87, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshihiko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/011763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258


```

1 REFERENCE/DOCKET NUMBER: 53466/184
2 TELECOMMUNICATION INFORMATION:
3 TELEPHONE: (202)672-5300
4 TELEFAX: (202)672-5399
5 TELEX: 904136
6 INFORMATION FOR SEQ ID NO: 87:
7 SEQUENCE CHARACTERISTICS:
8 LENGTH: 126 amino acids
9 TYPE: amino acid
10 TOPOLOGY: linear
11 MOLECULE TYPE: protein
12 US-08-646-265A-87
13
14 Query Match 89.8%; Score 502; DB 4; Length 126;
15 Best Local Similarity 89.7%; Pred. No. 5.6e-40;
16 Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0.
17
18 QY 1 DIQMSPSSLSASGDRVTITCKASONGTVNAVYQOKPGKAPRALYSASFIVGVPY 60
19 |||||
20 DIQMSPSSLSASGDRVTITCKASONGTVNAVYQOKPGSPPLISAYRISGVPS 79
21 |||||
22 QY 61 RFGSGSGTDFLTITSLDPEDFARYYCOQNYIPLTFEGGTRKVEIK 107
23 |||||
24 80 RFGSGSGTDFLTITSLDPEDFARYYCOQNYIPLTFEGGTRKVEIK 126
25 |||||
26 Db 80 RFGSGSGTDFLTITSLDPEDFARYYCOQNYIPLTFEGGTRKVEIK 126
27 |||||
28
29 RESULT 14
30 US-08-646-265A-59
31 Sequence 59, Application US/08646265A
32 Patent No. 6214973
33 GENERAL INFORMATION:
34 APPLICANT: OHTOMO, Toshiniko
35 APPLICANT: SATO, Koh
36 APPLICANT: TSUCHIYA, Masayuki
37 TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
38 TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
39 NUMBER OF SEQUENCES: 132
40 CORRESPONDENCE ADDRESS:
41 ADDRESSEE: Foley & Lardner
42 STREET: 3000 K Street, N.W., Suite 500
43 CITY: Washington
44 STATE: D.C.
45 COUNTRY: USA
46 ZIP: 20007-5109
47 COMPUTER READABLE FORM:
48 MEDIUM TYPE: Floppy disk
49 COMPUTER: IBM PC compatible
50 OPERATING SYSTEM: PC-DOS/MS-DOS
51 SOFTWARE: Patentin Release #1.0, Version #1.30
52 CURRENT APPLICATION DATA:
53 APPLICATION NUMBER: US/08/646,265A
54 FILING DATE: 09-SEP-1996
55 CLASSIFICATION: 435
56 PRIOR APPLICATION DATA:
57 APPLICATION NUMBER: WO PCT/JP94/01763
58 FILING DATE: 19-OCT-1994
59 PRIOR APPLICATION DATA:
60 APPLICATION NUMBER: JP 5-291078
61 FILING DATE: 19-NOV-1993
62 ATTORNEY/AGENT INFORMATION:
63 NAME: WEGNER, Harold C.
64 REGISTRATION NUMBER: 25,258
65 REFERENCE/DOCKET NUMBER: 53466/184
66 TELECOMMUNICATION INFORMATION:
67 TELEPHONE: (202)672-5300
68 TELEFAX: (202)672-5399
69 TELEX: 904136
70 INFORMATION FOR SEQ ID NO: 59:
71 SEQUENCE CHARACTERISTICS:
72 LENGTH: 126 amino acids
73 TYPE: amino acid
74 TOPOLOGY: linear
75 MOLECULE TYPE: protein

```

Query Match	89.4%;	Score 500;	DB 4;	Length 126;
Best Local Similarity	88.8%;	Pred. No. 8.6e-40;		
Matches 95; Conservative	4;	Mismatches 8;	Indels 0;	Gaps 0;
DB				
1 DIOMQSPSSLSASVGDRTITCKASONGTNAVWYOOKPGKAPALITYSASFLYGVPY 60				
20 DIOMQSPSSLSASVGDRTITCKASONGTNAVWYOOKPGKAPALITYSASFLYGVPY 79				
QY				
61 RRSQSGSGTDFLTITSLQPEDFATYCCQYNIYPLTEGQGRKVEIK 107				
DB				
80 RRSQSGSGTDFLTITSLQPEDFATYCCQYNIYPLTEGQGRKVEIK 126				
RESULT 15				
US-08-646-265A-75				
Sequence 75; Application US/08646265A				
Patent No. 6214973				
GENERAL INFORMATION:				
APPLICANT: OHTOMO, Toshiniko				
APPLICANT: SATO, Koh				
APPLICANT: TSUCHIYA, Masayuki				
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN				
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS				
NUMBER OF SEQUENCES: 132				
CORRESPONDENCE ADDRESS:				
ADDRESSEE: Foley & Lardner				
STREET: 3000 K Street, N.W., Suite 500				
CITY: Washington				
STATE: D.C.				
COUNTRY: USA				
ZIP: 20007-5109				
COMPUTER READABLE FORM:				
MEDIUM TYPE: Floppy disk				
COMPUTER: IBM PC compatible				
OPERATING SYSTEM: PC-DOS/MS-DOS				
SOFTWARE: PatentIn Release #1.0, Version #1.30				
CURRENT APPLICATION DATA:				
APPLICATION NUMBER: US/08/646.265A				
FILING DATE: 09-SEP-1996				
CLASSIFICATION: 435				
PRIOR APPLICATION DATA:				
APPLICATION NUMBER: WO PCT/JP94/01763				
FILING DATE: 19-OCT-1994				
PRIOR APPLICATION DATA:				
APPLICATION NUMBER: JP 5-291078				
FILING DATE: 19-NOV-1993				
ATTORNEY/AGENT INFORMATION:				
NAME: WEGNER, Harold C.				
REGISTRATION NUMBER: 25,258				
REFERENCE/DOCKET NUMBER: 53466/184				
TELECOMMUNICATION INFORMATION:				
TELEPHONE: (202)672-5300				
TELEFAX: (202)672-5399				
TELEX: 904136				
INFORMATION FOR SEQ ID NO: 75:				
SEQUENCE CHARACTERISTICS:				
LENGTH: 126 amino acids				
TYPE: amino acid				
TOPOLOGY: linear				
MOLECULE TYPE: protein				
US-08-646-265A-75				
Query Match	89.1%;	Score 498;	DB 4;	Length 126;
Best Local Similarity	88.8%;	Pred. No. 1.3e-39;		
Matches 95; Conservative	4;	Mismatches 8;	Indels 0;	Gaps 0;
QY				
1 DIOMQSPSSLSASVGDRTITCKASONGTNAVWYOOKPGKAPALITYSASFLYGVPY 60				
20 DIOMQSPSSLSASVGDRTITCKASONGTNAVWYOOKPGKAPALITYSASFLYGVPY 79				
QY				
61 RRSQSGSGTDFLTITSLQPEDFATYCCQYNIYPLTEGQGRKVEIK 107				

Db 80 RPSGSGSTDFTLTTLSSLOPEDIDYFCQOYNSTPRAGGTKEIK 126

Search completed: April 2, 2003, 14:40:36
Job time : 29 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 2, 2003, 14:39:14 ; Search time 34 Seconds
(Without alignments)
192.399 Million cell updates/sec

Title: US-09-875-221B-9

Perfect score: 559

Sequence: 1 DIOMTOSPSLSASVGDRTV.....COQYNYPLFRGQGTKEIK 107

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCR_NEM_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEM_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/US10_NEM_PUB.pep:*
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13: /cgn2_6/ptodata/2/pubpaa/US60_NEM_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	559	100.0	107	9	US-09-875-221A-9
2	559	100.0	107	9	US-09-949-559-9
3	559	100.0	214	9	US-09-875-221A-128
4	559	100.0	214	10	US-09-949-559-128
5	554	99.1	107	9	US-09-875-221A-11
6	554	99.1	107	10	US-09-949-559-11
7	520	93.0	107	10	US-09-905-243-77
8	513	91.8	126	9	US-09-749-873-65
9	509	91.1	107	9	US-09-749-873-130
10	509	91.1	126	9	US-09-749-873-43
11	509	91.1	126	9	US-09-749-873-91
12	509	91.1	269	9	US-09-749-873-109
13	506	90.5	126	9	US-09-749-873-47
14	505	90.3	126	9	US-09-749-873-51
15	504	90.2	126	9	US-09-749-873-57
16	504	90.2	126	9	US-09-749-873-63
17	502	89.8	107	9	US-09-749-873-131
18	502	89.8	126	9	US-09-749-873-53
19	502	89.8	126	9	US-09-749-873-85

20	502	89.8	126	9	US-09-749-873-87	Sequence 87, Appl
21	500	89.4	126	9	US-09-749-873-59	Sequence 59, Appl
22	498	89.1	126	9	US-09-749-873-75	Sequence 75, Appl
23	497	88.9	102	10	US-09-905-243-80	Sequence 80, Appl
24	497	88.9	109	10	US-09-811-123-5	Sequence 5, Appl
25	497	88.9	126	9	US-09-749-873-69	Sequence 69, Appl
26	497	88.9	126	9	US-09-749-873-77	Sequence 77, Appl
27	491	87.8	126	9	US-09-749-873-73	Sequence 73, Appl
28	484	86.6	126	9	US-09-749-873-81	Sequence 81, Appl
29	481	86.0	108	10	US-09-971-543-7	Sequence 7, Appl
30	481	86.0	252	10	US-09-971-543-1	Sequence 1, Appl
31	474	84.8	108	10	US-09-056-160B-12	Sequence 12, Appl
32	474	84.8	109	10	US-09-811-123-6	Sequence 6, Appl
33	472	84.4	108	9	US-09-875-221A-104	Sequence 104, App
34	472	84.4	108	9	US-09-949-559-104	Sequence 104, App
35	469	83.9	107	9	US-10-035-637-2	Sequence 2, Appl
36	466	83.4	126	9	US-09-269-921-106	Sequence 106, App
37	466	83.4	126	10	US-09-760-723-6	Sequence 6, Appl
38	466	83.4	126	10	US-09-355-925-6	Sequence 6, Appl
39	464.5	83.1	109	9	US-09-726-258-47	Sequence 47, Appl
40	464	83.0	105	10	US-09-974-449-4	Sequence 4, Appl
41	464	83.0	211	10	US-09-974-449-36	Sequence 36, Appl
42	463	82.8	108	9	US-09-910-483-3	Sequence 3, Appl
43	463	82.8	108	9	US-09-910-483-7	Sequence 7, Appl
44	463	82.8	108	9	US-09-910-483-11	Sequence 11, Appl
45	463	82.8	108	9	US-09-910-483-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1

US-09-875-221A-9

Sequence 9, Application US/09875221A

Publication No. US20030026805A1

GENERAL INFORMATION:

APPLICANT: Athwal, Diljeet Singh

APPLICANT: Brown, Derek Thomas

APPLICANT: Weir, Andrew Neil Charles

APPLICANT: Popplewell, Andrew George

APPLICANT: Chapman, Andrew Paul

APPLICANT: King, David John

TITLE OF INVENTION: Biological Products

FILE REFERENCE: Carp-0089

CURRENT APPLICATION NUMBER: US/09/875,221A

CURRENT FILING DATE: 2001-06-06

PRIOR APPLICATION NUMBER: GB0013810.7

PRIOR FILING DATE: 2000-06-06

NUMBER OF SEQ ID NOS: 130

SOFTWARE: PatentIn version 3.1

SEQ ID NO 9

LENGTH: 107

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: htf40-gli

US-09-875-221A-9

Query Match 100.0%; Score 559; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 5e-34;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIOMTOSPSLSASVGDRTVCKASQNGTVNAVYQCKRGAAPRALIYSASFILYSGVPY 60

DB 1 DIOMTOSPSLSASVGDRTVCKASQNGTVNAVYQCKRGAAPRALIYSASFILYSGVPY 60

QY 61 RSSGSGSGTDFLTITSSLOPEDFATYYCOQYNYPLFRGQGTKEIK 107

DB 61 RSSGSGSGTDFLTITSSLOPEDFATYYCOQYNYPLFRGQGTKEIK 107

QY 61 RSSGSGSGTDFLTITSSLOPEDFATYYCOQYNYPLFRGQGTKEIK 107

DB 61 RSSGSGSGTDFLTITSSLOPEDFATYYCOQYNYPLFRGQGTKEIK 107

RESULT 2
US-09-949-559-9

Sequence 9, Application US/09949559
Patent No. US20020151682A1
GENERAL INFORMATION:
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Brown, Derek Thomas
APPLICANT: Weir, Andrew Neil Charles
APPLICANT: Popplewell, Andrew George
APPLICANT: Chapman, Andrew Paul
APPLICANT: King, David John
TITLE OF INVENTION: Biological Products
FILE REFERENCE: Carp-0095
CURRENT APPLICATION NUMBER: US/09/949,559
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 0013810.7GB
PRIOR FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: 09/875,221
PRIOR FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: hTF40-gL1
US-09-949-559-9

Query Match 100.0%; Score 559; DB 10; Length 107;
Best Local Similarity 100.0%; Pred. No. 5e-34;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIOMTQSPSSLSASVGDRTYITCKASQNGTNAVWYQQRKAPKALISASFLYSGVPY 60
Db 1 DIOMTQSPSSLSASVGDRTYITCKASQNGTNAVWYQQRKAPKALISASFLYSGVPY 60
Qy 61 RFSGSGSGDTFTLTISSLQPEDFATYYCOQYNITPLTFGGGTVEIK 107
Db 61 RFSGSGSGDTFTLTISSLQPEDFATYYCOQYNITPLTFGGGTVEIK 107

RESULT 3
US-09-875-221A-128
Sequence 128, Application US/09875221A
Publication No. US20030026805A1
GENERAL INFORMATION:
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Brown, Derek Thomas
APPLICANT: Weir, Andrew Neil Charles
APPLICANT: Popplewell, Andrew George
APPLICANT: Chapman, Andrew Paul
APPLICANT: King, David John
TITLE OF INVENTION: Biological Products
FILE REFERENCE: Carp-0089
CURRENT APPLICATION NUMBER: US/09/875,221A
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: GB0013810.7
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PatentIn version 3.1
SEQ ID NO 128
LENGTH: 214
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Grafted light chain for fab and modified fab
US-09-875-221A-128

Query Match 100.0%; Score 559; DB 9; Length 214;
Best Local Similarity 100.0%; Pred. No. 8.8e-34;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIOMTQSPSSLSASVGDRTYITCKASQNGTNAVWYQQRKAPKALISASFLYSGVPY 60
Db 1 DIOMTQSPSSLSASVGDRTYITCKASQNGTNAVWYQQRKAPKALISASFLYSGVPY 60

Db 1 DIOMTQSPSSLSASVGDRTYITCKASQNGTNAVWYQQRKAPKALISASFLYSGVPY 60
Qy 61 RFSGSGSGDTFTLTISSLQPEDFATYYCOQYNITPLTFGGGTVEIK 107
Db 61 RFSGSGSGDTFTLTISSLQPEDFATYYCOQYNITPLTFGGGTVEIK 107

RESULT 4
US-09-949-559-128
Sequence 128, Application US/09949559
Patent No. US20020151682A1
GENERAL INFORMATION:
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Brown, Derek Thomas
APPLICANT: Weir, Andrew Neil Charles
APPLICANT: Popplewell, Andrew George
APPLICANT: Chapman, Andrew Paul
APPLICANT: King, David John
TITLE OF INVENTION: Biological Products
FILE REFERENCE: Carp-0095
CURRENT APPLICATION NUMBER: US/09/949,559
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 0013810.7GB
PRIOR FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: 09/875,221
PRIOR FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PatentIn version 3.1
SEQ ID NO 128
LENGTH: 214
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Grafted light chain for fab and modified fab
US-09-949-559-128

Query Match 100.0%; Score 559; DB 10; Length 214;
Best Local Similarity 100.0%; Pred. No. 8.8e-34;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIOMTQSPSSLSASVGDRTYITCKASQNGTNAVWYQQRKAPKALISASFLYSGVPY 60
Db 1 DIOMTQSPSSLSASVGDRTYITCKASQNGTNAVWYQQRKAPKALISASFLYSGVPY 60
Qy 61 RFSGSGSGDTFTLTISSLQPEDFATYYCOQYNITPLTFGGGTVEIK 107
Db 61 RFSGSGSGDTFTLTISSLQPEDFATYYCOQYNITPLTFGGGTVEIK 107

RESULT 5
US-09-875-221A-11
Sequence 11, Application US/09875221A
Publication No. US20030026805A1
GENERAL INFORMATION:
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Brown, Derek Thomas
APPLICANT: Weir, Andrew Neil Charles
APPLICANT: Popplewell, Andrew George
APPLICANT: Chapman, Andrew Paul
APPLICANT: King, David John
TITLE OF INVENTION: Biological Products
FILE REFERENCE: Carp-0089
CURRENT APPLICATION NUMBER: US/09/875,221A
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: GB0013810.7
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

Qy 1 DIOMTQSPSSLSASVGDRTYITCKASQNGTNAVWYQQRKAPKALISASFLYSGVPY 60
Db 1 DIOMTQSPSSLSASVGDRTYITCKASQNGTNAVWYQQRKAPKALISASFLYSGVPY 60

OTHER INFORMATION: hnf40-gL2
US-09-875-221a-11

Query Match 99.1%; Score 554; DB 9; Length 107;
Best Local Similarity 99.1%; Pred. No. 1.1e-33;
Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVSGRVTITCKASQNVGTNVAWYQKPKAKALITYSFLYSGVPY 60
DB 1 DIOMTQSPSSLSASVSGRVTITCKASQNVGTNVAWYQKPKAKALITYSFLYSGVPY 60
QY 61 RFGSGSGTDFTLTISLQPEDFATYCCQYNYPLTFGGGTKEIK 107
DB 61 RFGSGSGTDFTLTISLQPEDFATYCCQYNYPLTFGGGTKEIK 107

RESULT 6
US-09-949-559-11

Sequence 11, Application us/09949559
Patent No. US20020151682A1

GENERAL INFORMATION:
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Brown, Derek Thomas
APPLICANT: Weir, Andrew Neil Charles
APPLICANT: Popplewell, Andrew George
APPLICANT: Chapman, Andrew Paul
TITLE OF INVENTION: Biological Products
FILE REFERENCE: Carp-0095
CURRENT APPLICATION NUMBER: US/09/949,559
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 0013810.7GB
PRIOR FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: 09/875,221
PRIOR FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 130
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: hnf40-gL2
US-09-949-559-11

Query Match 99.1%; Score 554; DB 10; Length 107;
Best Local Similarity 99.1%; Pred. No. 1.1e-33;
Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVSGRVTITCKASQNVGTNVAWYQKPKAKALITYSFLYSGVPY 60
DB 1 DIOMTQSPSSLSASVSGRVTITCKASQNVGTNVAWYQKPKAKALITYSFLYSGVPY 60
QY 61 RFGSGSGTDFTLTISLQPEDFATYCCQYNYPLTFGGGTKEIK 107
DB 61 RFGSGSGTDFTLTISLQPEDFATYCCQYNYPLTFGGGTKEIK 107

RESULT 7
US-09-905-243-77

Sequence 77, Application us/09905243
Patent No. US20020062009A1

GENERAL INFORMATION:
APPLICANT: Taylor, Alexander H
TITLE OF INVENTION: Monoclonal Antibodies with Reduced
FILE REFERENCE: P50770
CURRENT APPLICATION NUMBER: us/09/905,243
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/300,970
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 77
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: murine/chimpanzee sequence
US-09-905-243-77

Query Match 93.0%; Score 520; DB 10; Length 107;
Best Local Similarity 94.4%; Pred. No. 3.2e-31;
Matches 101; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVSGRVTITCKASQNVGTNVAWYQKPKAKALITYSFLYSGVPY 60
DB 1 DIOMTQSPSSLSASVSGRVTITCKASQNVGTNVAWYQKPKAKALITYSFLYSGVPY 60
QY 61 RFGSGSGTDFTLTISLQPEDFATYCCQYNSPLTFGGGTKEIK 107
DB 61 RFGSGSGTDFTLTISLQPEDFATYCCQYNSPLTFGGGTKEIK 107

RESULT 8
US-09-749-873-65

Sequence 65, Application us/09749873
Publication No. US20030023045A1
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshiniko
SATO, Koh
TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/749,873
FILING DATE: 29-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,265
FILING DATE: 1996-09-09
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399

INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-749-873-65

Query Match 91.8%; Score 513; DB 9; Length 126;
Best Local Similarity 92.5%; Pred. No. 1.2e-30;
Matches 99; Conservative 1; Mismatches 7; Indels 0; Gaps 0;


```

ADDRESS: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/749,873
FILING DATE: 29-Dec-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,265
FILING DATE: 1996-09-09
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 91:
US-09-749-873-91

Query Match          91.1%; Score 509; DB 9; Length 126;
Best Local Similarity 91.6%; Pred. No. 2.3e-30;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTITCKASQNGTVNAMYQOKPGKAPKALISASFLYGVY 60
Db 20 DIQMTQSPSSLSASVGDRTITCKASQNGTVNAMYQOKPGKAPKALISASFLYGVY 79
Qy 61 RFGSGSGTDFLTITSSLPEDFATYYCOQNYNYPLTFGQGTKEIK 107
Db 80 RFGSGSGTDFLTITSSLPEDFATYYCOQNYNSYPRAFGQGTKEIK 126

RESULT 12
US-09-749-873-109
Sequence 109, Application US/09/749873
Publication No. US20030023045A1
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshihiko
SATO, Koh
TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESS: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/749,873
FILING DATE: 29-Dec-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,265
FILING DATE: 1996-09-09
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 109:
US-09-749-873-109

Query Match          91.1%; Score 509; DB 9; Length 269;
Best Local Similarity 91.6%; Pred. No. 4.2e-30;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTITCKASQNGTVNAMYQOKPGKAPKALISASFLYGVY 60
Db 155 DIQMTQSPSSLSASVGDRTITCKASQNGTVNAMYQOKPGKAPKALISASFLYGVY 214
Qy 61 RFGSGSGTDFLTITSSLPEDFATYYCOQNYNYPLTFGQGTKEIK 107
Db 215 RFGSGSGTDFLTITSSLPEDFATYYCOQNYNSYPRAFGQGTKEIK 261

RESULT 13
US-09-749-873-47
Sequence 47, Application US/09/749873
Publication No. US20030023045A1
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshihiko
SATO, Koh
TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESS: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/749,873
FILING DATE: 29-Dec-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,265
FILING DATE: 1996-09-09
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.

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1  REGISTRATION NUMBER: 25, 258
2  REFERENCE/DOCKET NUMBER: 53466/184
3  TELECOMMUNICATION INFORMATION:
4  TELEPHONE: (202)672-5300
5  TELEFAX: (202)672-5399
6  TELEX: 904136
7  INFORMATION FOR SEQ ID NO: 47:
8  SEQUENCE CHARACTERISTICS:
9  LENGTH: 126 amino acids
10 TYPE: amino acid
11 TOPOLOGY: linear
12 MOLECULE TYPE: protein
13 SEQUENCE DESCRIPTION: SEQ ID NO: 47:
14 US-09-749-873-47
15
16 Query Match 90.5%; Score 506; DB 9; Length 126;
17 Best Local Similarity 90.7%; Pred. No. 3,7e-30;
18 Matches 97; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
19
20 1 DIQMTPSSSLASVAGDRTITCKASQNGTVWVYQOKPGKAPALITYSASFLYGVPY 60
21 20 DIQMTPSSSLASVAGDRTITCKASQNGTVWVYQOKPGKAPALITYSASFLYGV 79
22 61 RFGSGSGTDTFLTITSLQPEDFATYYCOQVNIYPLTSGGTKEIK 107
23 80 RFGSGSGTDTFLTITSLQPEDFATYYCOQVNSYPRAFQGTKEIK 126
24
25 RESULT 14
26 US-09-749-873-51
27 Sequence 51, Application US/09749873
28 Publication No. US20030023045A1
29 GENERAL INFORMATION:
30 APPLICANT: OHTOMO, Toshihiko
31 SATO, Koh
32 TSUCHIYA, Masayuki
33 TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
34 MEDULLOBLASTOMA CELLS
35 NUMBER OF SEQUENCES: 132
36 CORRESPONDENCE ADDRESS:
37 ADDRESSEE: Foley & Lardner
38 STREET: 3000 K Street, N.W., Suite 500
39 CITY: Washington
40 STATE: D.C.
41 COUNTRY: USA
42 ZIP: 20007-5109
43 COMPUTER READABLE FORM:
44 MEDIUM TYPE: floppy disk
45 COMPUTER: IBM PC compatible
46 OPERATING SYSTEM: PC-DOS/MS-DOS
47 SOFTWARE: PatentIn Release #1.0, Version #1.30
48 CURRENT APPLICATION DATA:
49 APPLICATION NUMBER: US/09/749,873
50 FILING DATE: 29-Dec-2000
51 CLASSIFICATION: <Unknown>
52 PRIOR APPLICATION DATA:
53 APPLICATION NUMBER: 08/646,265
54 FILING DATE: 1996-09-09
55 APPLICATION NUMBER: JP 5-291078
56 FILING DATE: 19-NOV-1993
57 ATTORNEY/AGENT INFORMATION:
58 NAME: WEGNER, Harold C.
59 REGISTRATION NUMBER: 25, 258
60 REFERENCE/DOCKET NUMBER: 53466/184
61 TELECOMMUNICATION INFORMATION:
62 TELEPHONE: (202)672-5300
63 TELEFAX: (202)672-5399
64 TELEX: 904136
65 INFORMATION FOR SEQ ID NO: 51:
66 SEQUENCE CHARACTERISTICS:
67 LENGTH: 126 amino acids
68 TYPE: amino acid
69 TOPOLOGY: linear

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: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-749-873-51

Query Match          90.3%, Score 505; DB 9; Length 126;
Best Local Similarity 90.7%; Pred. No. 4,4e-30;
Matches 97; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMOSPSSLSASVGDVYITTCRKSQNVGTVMVYQOKPGKAPKALITYSASFITYSGVPY 60
    |||||||
DB 20 DIQMOSPSSLSASVGDVYITTCRKSQNVGTVMVYQOKPGKAPKALITYSASFITYSGVPS 79
    |||||||

QY 61 RPSGSGCTDFLTITSLQPEDFATYTCQVNIYPLTFGQGTKEIK 107
    |||||||
DB 80 RPSGSGCTDFLTITSLQPEDIATYFCQVNSYPRAFQGTKEIK 126
    |||||||

RESULT 15
US-09-749-873-57
: Sequence 57, Application US/09749873
: Publication No. US20030023045A1
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshihiko
SAITO, KOJI
TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/749,873
FILING DATE: 29-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,265
FILING DATE: 1996-09-09
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-749-873-57

Query Match          90.2%, Score 504; DB 9; Length 126;
Best Local Similarity 89.7%; Pred. No. 5.2e-30;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMOSPSSLSASVGDVYITTCRKSQNVGTVMVYQOKPGKAPKALITYSASFITYSGVPY 60
    |||||||
DB 20 DIQMOSPSSLSASVGDVYITTCRKSQNVGTVMVYQOKPGKAPKALITYSASFITYSGVPS 79
    |||||||

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Thu Apr 3 08:53:30 2003

us-09-875-221b-9.rapb

Page 7

Oy 61 RFGSGGGTDTLTITSSLPEDFATYYCQYNIPLTFGQGTRVEIK 107
 |||||
 |||||
Db 80 RFSSGGGTDTFTTISLQPEDIATYYCQYNSTPRAGQGGRKVEIK 126

Search completed: April 2, 2003, 14:48:11
Job time : 35 secs

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 2, 2003, 14:35:09 ; Search time 43 Seconds
(without alignments)
239.218 Million cell updates/sec

Title: US-09-875-221b-9

Perfect score: 559

Sequence: 1 DIQMTGSPSSLSASVGDVRYT.....CQGYNYPLTFGCGTKVEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73:*
2: pir1:*
3: pir2:*
4: pir3:*
5: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	470	84.1	125	2	S40333	Ig kappa chain V-J
2	468	83.7	125	2	S40349	Ig kappa chain V-J
3	467	83.5	107	2	I69017	anti-HIV envelope
4	466	83.4	129	2	S40369	Ig kappa chain - h
5	462	82.6	108	1	K1HUBN	Ig kappa chain V-I
6	462	82.6	123	2	S40313	Ig kappa chain V-J
7	459	82.1	125	2	S40353	Ig kappa chain V-J
8	457	81.8	117	2	S46371	Ig kappa chain V-J
9	454	81.2	107	2	S36264	Ig kappa chain V
10	452	80.9	123	2	S40331	Ig kappa chain - h
11	451	80.7	108	2	B49047	Ig kappa chain V-I
12	450	80.5	108	1	K1HUBU	Ig kappa chain V-I
13	450	80.5	117	2	S46376	Ig kappa chain V-J
14	450	80.5	131	2	S40352	Ig kappa chain V-J
15	450	80.5	132	2	S40334	Ig kappa chain - h
16	448.5	80.2	124	2	S40336	Ig kappa chain V-J
17	448	80.1	108	2	S36279	Ig kappa chain V
18	447	80.0	108	2	S36277	Ig kappa chain V
19	446	79.8	107	2	S36269	Ig kappa chain V
20	446	79.8	108	1	K1HUGL	Ig kappa chain V-I
21	446	79.8	127	1	S40367	Ig kappa chain V-I
22	445	79.6	129	2	K1HUME	Ig kappa chain V-I
23	444	79.4	128	2	S40372	Ig kappa chain var
24	444	79.2	108	2	S19674	Ig kappa chain V-I
25	443	79.2	129	2	S52793	Ig kappa chain V-I
26	443	79.1	108	1	K1HOLY	Ig kappa chain V-I
27	442	78.8	107	2	S36275	Ig kappa chain V-I
28	440.5	78.7	108	1	K1HUEU	Ig kappa chain V-I
29	440	78.7	108	1	K1HUEU	Ig kappa chain V-I

30	439.5	78.6	107	1	K1HUR	Ig kappa chain V-I
31	438	78.5	132	2	S38646	Ig kappa chain V-I
32	438	78.4	129	2	S52789	Ig kappa chain V-I
33	437	78.2	107	2	S36262	Ig kappa chain V
34	437	78.2	124	2	S40318	Ig kappa chain V-I
35	435	77.8	125	2	S40316	Ig kappa chain - h
36	435	77.8	125	2	S40350	Ig kappa chain - h
37	435	77.8	127	2	S11240	Ig kappa chain V-I
38	434	77.6	108	1	K1HUBU	Ig kappa chain V-I
39	434	77.6	126	2	S40335	Ig kappa chain V-I
40	434	77.6	130	2	S40368	Ig kappa chain V-I
41	433.5	77.5	107	2	S47183	Ig kappa chain - h
42	433	77.5	108	2	S44122	Ig kappa chain V-I
43	433	77.5	122	2	S40370	Ig kappa chain V-I
44	432.5	77.4	108	2	S30521	Ig kappa chain V-I
45	432	77.3	108	1	K1HURU	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

S40333
Ig kappa chain V-J region - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40333

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40333

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-125 <KLE>

A:Cross-references: EMBL:X72443; NID:9441354; PIDN:CAA5111.1; PID:9441355

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-108/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 470; DB 2; Length 125;

Best Local Similarity 84.1%; Pred. No. 1e-33;

Matches 90; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTGSPSSLSASVGDVRYTTCASQNGVNVAMYOOKPKAKRLIYSASFYSGVPY 60

DB 19 DIQMTGSPSSLSASVGDVRYTTCASQISWLMAYOOPKAKRLIYSASFYSGVPS 78

QY 61 RFSGSGSTDEFTLTISLQPEDFATYVYCOQYNYPLTFGCGTKVEIK 107

DB 79 RFSGSGSTDEFTLTISLQPEDFATYVYCOQYNSYPMWTFGCGTKVEIK 125

RESULT 2

S40349
Ig kappa chain V-J region - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

C:Accession: S40349

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40349

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-125 <KLE>

A:Cross-references: EMBL:X72459; NID:9441386; PIDN:CAA51127.1; PID:9441387

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:35-107/Domain: immunoglobulin homology <IMM>

Query Match 83.7%; Score 468; DB 2; Length 125;

Best Local Similarity 84.9%; Pred. No.1.5e-33;
Matches 90; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

OY 2 IOMTQSPSSLSASVGDRTVTTCRASQNGTVNAMYQQKPKAKPALIYSASFLYSGVPYR 61
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 19 IQLTNQSPSSLSASVGDRVTITCRASQIGISALAWQQKPKAPKLLIIDASSLESGVPSR 78

OY 62 FSGSGSGDTFTLTISLQPEDFATYYCQGYNIYPLTFEGGKTVEIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 79 FSGSGSGDTFTLTISLQPEDFATYYCQGFNTYPLTFEGGKTVEIK 124

RESULT 3
169017
anti-HIV1 envelope protein gp120 V3 loop monoclonal antibody L chain V region - human (Ft
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
C:Accession: 169017
R:Chun, L.T.; Duenas, M.; Levi, M.; Hinkula, J.; Mahren, B.; Borrebaeck, C.A.
Immunol. Lett. 44, 25-30, 1995
A>Title: Molecular characterization of a human anti-HIV 1 monoclonal antibody revealed a
A:Reference number: 154563; MUID:95237884; PMID:7721339
A:Accession: 169017
A>Status: preliminary; translated from GB/EMBL/DDBU
A:Molecule type: mRNA
A:Residues: 1-107 <RSS>
A:Cross-references: GB:S77140; NID:g913352; PIDN:AAB34102.1; PID:g913353
C:Genetics:
A:Gene: Ig Vkappa
C:Superfamily: Immunoglobulin V region: immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.5%; Score 467; DB 2; Length 107;
Best Local Similarity 83.2%; Pred. No.1.6e-33;
Matches 89; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

OY 1 DIOMTQSPSSLSASVGDVTTTCRASQNGTVNAMYQQKPKAKPALIYSASFILXGVYP 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIOYTQSPSSLSASVGDVTTTCRASHDIGSYLAMWQQKPKAPESLIYAASSLQSGVPS 60

OY 61 RFSGSGSGDTFTLTISLQPEDFATYYCQGYNIYPLTFEGGKTVEIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFSGSGSGDTFTLTISLQPEDFATYYCQGYNSVPIITFGGTVKLIK 107

RESULT 4
S40369
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40369
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40369
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-129 <KIE>
A:Cross-references: EMBL:X72479; NID:g441426; PIDN:CAA51147.1; PID:g441427
C:Superfamily: immunoglobulin V region: immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 83.4%; Score 466; DB 2; Length 129;
Best Local Similarity 82.2%; Pred. No.2.3e-33;
Matches 88; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

OY 1 DIOMTQSPSSLSASVGRVTTTCRASQNGTVNAMYQQKPKAPKALIYSASFXYGVPY 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 22 DIOMTQSPSSLSASVGRVTTTCRASHSIHMLYWFOQKPKAKAKSLIIYAASSLQSGVPS 81

OY 61 RFSGSGSGDTFTLTISLQPEDFATYYCQGYNIYPLTFEGGKTVEIK 107

[illegible]

Dd 17 DIQMTQSPSSLSASVGRVTITTCRASTGGIIRNDLAFNQQPKCAPRRLITYDAASLLSGVPS 76

Qy 61 RFGSGSGTDFLTITSLQPDPEDFATYYCQYMIYPLTREGGKRVK 107
|||||::||| ||||| ||| ||| ||| ||| |||
Db 77 RFGSGSGTEFTLTISLPQDPEDFATYYCYLQNYGRTGGGKRVK 123

RESULT 7

Ig kappa chain V-J-C region - human
 C:Species: Homo sapiens (man)
 C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S40353
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A:Title: Expressed human immunoglobulin chi genes and their hypermutation
 A:Reference number: S40312; MUID:94080891; PMID:8258341
 A:Accession: S40353
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-125 <KLE>
 A:Cross-references: EMBL:X72463
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:30-104/Domain: immunoglobulin homology <IMM>

Query Match	82.1%	Score 459	DB 2	length 125
Best Local Similarity	81.3%	Pred. No. 9	1e-33	
Matches 87	Conservative	8	Mismatches 12	Indels 0
			Gaps	0

[illegible]

RESULT 8

Ig kappa chain V-J region (T24-3) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
 C:Accession: S46371; S38645
 R:Bensimon, C.; Chastagner, P.; Zouali, M.
 EMO J. 13, 2951-2962, 1994
 A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene ree
 A:Reference number: S46369; MUID:94313975; PMID:8039491
 A:Accession: S46371
 A:Molecule type: mRNA
 A:Residues: 1-117 <BEN>
 A:Cross-references: EMBL:Z27172; NID:9415959; PIDN:CAAB1696.1; PID:9415960
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 C:Keywords: Domain: immunoglobulin homology <IMX>
 C:23-97/Domain: immunoglobulin homology

Query Match	81.8%	Score 457	DB 2:	Length 117
Best Local Similarity	81.7%	Pred. No. 1.3e-32		
Matches 89; Conservative	9;	Mismatches 9;	Indels 2;	Gaps 1;

[illegible]

RESULT 9

Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)

C.Species: Homo sapiens (man)
C.Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C.Accession: S36264
C.Griffiths, A.D.: Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A.Title: Human anti-self antibodies with high specificity from phage display library
A.Reference number: S36256; MUID:93178448; PMID:7679990
A.Accession: S36264

Query Match	81.2%	Score 454	DB 2	Length 107
Best Local Similarity	81.3%	Pred. No. 2.1e-32		
Matches 87	Conservative 10	Mismatches 10	Indels 0	Gaps 0

OY	1	D1OMQSPSLSASVGDRTITCRKASONGTVNVAWQKPGAPALIIYASAFILXGVY	60
		: : : : : : : : : : : : : : : : : :	
		: : : : : : : : : : : : : : : : : :	
Db	1	EIVLHQSPSLSASVGDRTITCRASQSISTVLNMVQQKRGAKPLIITYAASIASGVP	60
		: : : : : : : : : : : : : : : : : :	
		: : : : : : : : : : : : : : : : : :	
OY	61	RSSGSSTGDTFLTISSLOPEPFIATYYCOQNYITPLETGGCKRVEK	107
		: : : : : : : : : : : : : : : : : :	
		: : : : : : : : : : : : : : : : : :	
Db	61	RSSGSSTGDTFLTISSLOPEPFIATYYCOQNYITPLETGGCKRVKIDK	107

RESULT 10

Ig kappa chain - human
C.Species: Homo sapiens (man)
C.Date: 06-Mar-1994 #sequence-revision 26-May-1995 #text-change 21-Jan-2000
C.Accession: S40331
R.Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A.Title: Expressed human immunoglobulin chi genes and their hypermutation.
A.Reference number: S40331; MUID:94080891; PMID:8258341
A.Accession: S40331
A.Status: preliminary; translation not shown
A.Molecule type: mRNA
A.Residues: 1-123 <KME>
A.CROSS-references: EMBL:X72441; MID:g9441350; PIDN:CA51109.1; PID:g441351
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
F:32-106/Domain: immunoglobulin homology <IMM>

Query Match	80.9%	Score 452	DB 2	Length 123
Best Local Similarity	83.2%	Pred. No. 3.6e-32		
Matches 89, Conservative		6, Mismatches 12	Indels 0	Gaps 0

Qy	1	DDMMSPSSLSASVGDPRITICKASONGVWVWVWQKRGKAPRLIYASAFITGVGY	60
Qy		: : : : : : : : :	
Db	17	DIQMTPSSLSASVGDPRITICKASQSISLITNNYQKRGKAPRLIYAAASLSQGVPS	76
Qy	61	RFSGSGSGTDFLTLLTSLDPEDFATYVCOQYNIYPLTRSGQTKVEIK	107
Qy		: : : : : : : :	
Db	77	RFSGSGSGTDFLTLLTSLDPEDFATYVCOQYSTPTPEQSGTKVEIK	123
Qy		: : : : : : : :	

RESULT 11

ig kappa chain V region (monoclonal strational autoantibody StrAB SA-1A) - human (fr
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B49047
R:Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A:Title: Human monoclonal strational autoantibodies isolated from thymic B lymphocytes
A:Reference number: A49047; MUID:92387224; PMID:151616
A:Accession: B49047
A:Status: preliminary

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GenCore version 5.1.4.D5_4578
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OM protein - protein search, using sw model

Run on: April 2, 2003, 14:28:14 ; Search time 24 Seconds

(Without alignments)
184.915 Million cell updates/sec

Title: US-09-875-221B-9

Perfect score: 559

Sequence: 1 DIQMTQSPSSLSASVGRVT.....COQYNIPYLPFGQGTQVEIK 107

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SWISSProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	462	82.6	108	1	KV1V_HUMAN
2	450	80.5	108	1	KV1H_HUMAN
3	446	79.8	108	1	KV1G_HUMAN
4	445	79.6	108	1	KV1R_HUMAN
5	442	79.1	108	1	KV1M_HUMAN
6	440	78.7	108	1	KV1F_HUMAN
7	439.5	78.6	107	1	KV1D_HUMAN
8	439	78.5	108	1	KV1Y_HUMAN
9	434	77.6	108	1	KV1B_HUMAN
10	432	77.3	108	1	KV1L_HUMAN
11	429	76.7	108	1	KV1P_HUMAN
12	427	76.4	108	1	KV1S_HUMAN
13	425	76.0	108	1	KV1Q_HUMAN
14	423	75.7	108	1	KV1O_HUMAN
15	423	75.7	129	1	KV1C_HUMAN
16	420	75.1	108	1	KV1G_HUMAN
17	419	75.0	108	1	KV1A_HUMAN
18	418	74.8	108	1	KV1E_HUMAN
19	416	74.4	108	1	KV1I_HUMAN
20	416	74.4	117	1	KV1N_HUMAN
21	415	74.2	108	1	KV1J_HUMAN
22	409	73.2	117	1	KV1J_HUMAN
23	402	71.9	129	1	KV1X_HUMAN
24	398	71.2	149	1	KV5A_MOUSE
25	387.5	69.3	109	1	KV1T_HUMAN
26	387	69.2	112	1	KV1U_HUMAN
27	386	69.1	108	1	KV5J_MOUSE
28	385.5	69.0	129	1	KV3H_HUMAN
29	384.5	68.8	129	1	KV3L_HUMAN
30	382	68.3	108	1	KV5Q_MOUSE
31	381	68.2	108	1	KV5T_MOUSE
32	381	68.2	128	1	KV5E_MOUSE
33	379	67.8	108	1	KV5S_MOUSE

34	378.5	67.7	109	1	KV3D_HUMAN	P01622	homo sapien
35	377.5	67.5	129	1	KV3M_HUMAN	P18136	homo sapien
36	377	67.4	108	1	KV5D_MOUSE	P01636	mus musculus
37	376	67.3	134	1	KV4C_HUMAN	P06314	homo sapien
38	375.5	67.2	109	1	KV3E_HUMAN	P01624	homo sapien
39	373.5	66.8	109	1	KV3E_HUMAN	P01624	homo sapien
40	373	66.7	108	1	KV5P_MOUSE	P01649	mus musculus
41	372	66.5	114	1	KV4A_HUMAN	P01625	homo sapien
42	372	66.5	136	1	KV5B_MOUSE	P01634	mus musculus
43	371	66.4	108	1	KV5L_MOUSE	P01645	mus musculus
44	371	66.4	108	1	KV5R_MOUSE	P01651	mus musculus
45	370.5	66.3	109	1	KV3E_HUMAN	P01623	homo sapien

ALIGNMENTS

RESULT 1		ALIGNMENTS	
ID	Query Match	Score	DB 1; Length 108;
KV1V_HUMAN	Best Local Similarity 82.6%; Pred. No. 1.4e-41;	Matches 89; Conservative 7; Mismatches 11; Indels 0; Gaps 0;	
KV1V_HUMAN	Standard; PRT; 108 AA.		
AC	P04430;		
DT	13-AUG-1987 (Rel. 05, Created)		
DT	13-AUG-1987 (Rel. 05, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	Ig kappa chain V-1 region BAN.		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
ON	[1]		
RP	SEQUENCE.		
RX	MEDLINE=86174817; PubMed=3083240;		
RA	Dwulet F.E., O'Connor T.P., Benson M.D.;		
RT	"Polymorphism in a kappa I primary (Al) amyloid protein (BAN).";		
RI	MOL. Immunol. 23:73-78(1986).		
DR	PIR; A01878; K1HUBN.		
DR	HSSP; P80362; 1MTL.		
DR	InterPro: IPR003596; Ig_MHC.		
DR	InterPro: IPR003596; Ig_v.		
DR	Pfam; PF00047; Ig_1.		
DR	SMART; SM00406; Ig; 1.		
KW	Immunoglobulin V region; Amyloid.		
FT	DOMAIN 1 23		
FT	DOMAIN 24 34		
FT	DOMAIN 35 49		
FT	DOMAIN 50 56		
FT	DOMAIN 57 88		
FT	DOMAIN 89 97		
FT	DOMAIN 98 107		
FT	DISULFID 23 88		
FT	NON_TER 108		
SQ	SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;		
Query Match			
Best Local Similarity 82.6%; Pred. No. 1.4e-41;			
Matches 89; Conservative 7; Mismatches 11; Indels 0; Gaps 0;			
QY	1 DIQMTQSPSSLSASVGRVTITCKASQNYGVNAYTQQRKAPKALITISAFISGVY 60		
DB	1 DIQMTQSPSSLSASVGRVTITCKASQNYGVNAYTQQRKAPKALITISAFISGVY 60		
QY	61 RFSGSGGTDFLTITSLQPEDFATYYCOQYNIPYLPFGQGTQVEIK 107		
DB	61 RFSGSGGTDFLTITSLQPEDFATYYCOQYNIPYLPFGQGTQVEIK 107		
RESULT 2			
ID	KV1H_HUMAN	Standard; PRT; 108 AA.	
AC	P01600;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		

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DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN NCB1_TaxID=9606;
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT subgroups."
RL Hoppe-Sejler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR HSSP; A01868; KIHUHU.
DR PIR; A01868; KIHUHU.
DR HSSP; P80362; IWTU.
DR InterPro; IPR003596; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR Pfam; PF00047; IGV; 1.
DR Immunoglobulin V region; Bence-Jones protein.
KW DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A61608D0618 CRC64;

Query Match 80.5%; Score 450; DB 1; Length 108;
Best Local Similarity 81.3%; Pred. No. 2.4e-40;
Matches 87; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTVITTCASQNVGTNNAWYQOKRGKAPKALITYASFLYSVPY 60
DB 1 DIOMTQSPSSLSASVGDRTVITTCASQNVGTNNAWYQOKRGKAPKALITYASFLYSVPY 60
QY 61 RFSGSGSGTDFTLTISLQPEDFATYYCCQYNYIPLTFGGGTVEIK 107
DB 61 RFSGSGSGTDFTLTISLQPEDFATYYCCQYNYIPLTFGGGTVEIK 107

RESULT 3
KVIG_HUMAN STANDARD; PRT; 108 AA.
AC P01599;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region GAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN NCB1_TaxID=9606;
RP SEQUENCE.
RX MEDLINE=75059122; PubMed=4215718;
RA Laure C.J., Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal Igm-immunoglobulin
RT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
RT kappa-type, subgroup I."
RL Hoppe-Sejler's Z. Physiol. Chem. 354:1503-1504(1973).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR; A01867; KIHUHL.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.

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DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
RN NCB1_TaxID=9606;
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT subgroups."
RL Hoppe-Sejler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR HSSP; A01868; KIHUHU.
DR PIR; A01868; KIHUHU.
DR HSSP; P80362; IWTU.
DR InterPro; IPR003596; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Bence-Jones protein.
KW DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FE73 CRC64;

Query Match 79.8%; Score 446; DB 1; Length 108;
Best Local Similarity 80.4%; Pred. No. 6.4e-40;
Matches 86; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTVITTCASQNVGTNNAWYQOKRGKAPKALITYASFLYSVPY 60
DB 1 DIOMTQSPSSLSASVGDRTVITTCASQNVGTNNAWYQOKRGKAPKALITYASFLYSVPY 60
QY 61 RFSGSGSGTDFTLTISLQPEDFATYYCCQYNYIPLTFGGGTVEIK 107
DB 61 RFSGSGSGTDFTLTISLQPEDFATYYCCQYNYIPLTFGGGTVEIK 107

RESULT 4
KVIR_HUMAN STANDARD; PRT; 108 AA.
AC P01610;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN NCB1_TaxID=9606;
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal Igm
RT (protein WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33."
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
DR PIR; A01876; KIHUWE.
DR HSSP; P80362; IWTU.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Monoclonal antibody.
KW DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Query Match 79.6%; Score 445; DB 1; Length 108;
Best Local Similarity 78.5%; Pred. No. 8.2e-40;
Matches 84; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTVITTCASQNVGTNNAWYQOKRGKAPKALITYASFLYSVPY 60

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DR HSSP; P80362; 1MTL.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region; Glycoprotein.
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .).
 FT NON_TER 107 107
 SQ SEQUENCE 107 AA; 11703 MW; 11BPDP9844C3346 CRC64;

Query Match 78.6%; Score 439.5; DB 1; Length 107;
 Best Local Similarity 78.5%; Pred. No. 3e-39;
 Matches 84; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

QY 1 DIQMTQSPSSLSASVDGVITTCASQNVGTNVAWYQOKPGKAPKALISAFLYSGVPY 60
 DB 1 DIQMTQSPSSLSASVDGVITTCASQNVGTNVAWYQOKPGKAPKALISAFLYSGVPY 60
 QY 61 RFGSGSGTDFLTITISLPEDFATYYCOQYNIYPLTFGGGTVEIK 107
 DB 61 RFGSGSGTDFLTITISLPEDFATYYCOQYNIYPLTFGGGTVEIK 106

RESULT 8

KVIL_HUMAN STANDARD; PRT; 108 AA.
 ID KVIL_HUMAN
 AC P80362;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region MAT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP MEDLINE-95086080; PubMed-7993911;
 RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
 RA Solomon A., Stevens F.J., Schiffer M.;
 RT "Comparison of crystal structures of two homologous proteins:
 RT structural analysis of altered domain interactions in immunoglobulin
 RT light-chain dimers."
 RL Biochemistry 33:14648-14657(1994).

RN [2]
 RP SEQUENCE OF 1-35.
 RX MEDLINE-8167384; PubMed-6167731;
 RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
 RA Popp R.A., Solomon A.;
 RT "Characterization and preliminary crystallographic data on the VL-
 RT related fragment of the human kappa Bence Jones protein Mat."
 RL J. Mol. Biol. 147:185-193(1981).
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PDB: 1MTL; 01-NOV-94.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; IGV; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 FRAMEWORK-2.
 FT DOMAIN 35 49 FRAMEWORK-3.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 107 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT CONFLICT 30 31 TN -> SD (IN REF. 2).
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE97 CRC64;

Query Match 78.5%; Score 439; DB 1; Length 108;
 Best Local Similarity 78.5%; Pred. No. 3.5e-39;

Matches 84; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGVITTCASQNVGTNVAWYQOKPGKAPKALISAFLYSGVPY 60
 DB 1 DIQMTQSPSSLSASVDGVITTCASQNVGTNVAWYQOKPGKAPKALISAFLYSGVPY 60
 QY 61 RFGSGSGTDFLTITISLPEDFATYYCOQYNIYPLTFGGGTVEIK 107
 DB 61 RFGSGSGTDFLTITISLPEDFATYYCOQYNIYPLTFGGGTVEIK 107

RESULT 9

KVIL_HUMAN STANDARD; PRT; 108 AA.
 ID KVIL_HUMAN
 AC P01594;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region AU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-72189444; PubMed-5028201;
 RA Schlecht H., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
 RT protein Au)."
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).

RN [2]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE-77022433; PubMed-1234024;
 RA Felhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
 RA Schwager P., Steigemann W., Schramm H.J.;
 RT "The structure determination of the variable portion of the
 RT Bence-Jones protein Au."
 RL Biophys. Struct. Mech. 1:139-146(1975).
 CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
 CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
 CC REGION OF THE KAPPA CHAIN REI.
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR: A01862; KIHUWU.
 DR HSSP: P01607; IRET.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; IGV; 1.
 DR SMART: SM00406; IGV; 1.

KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 FRAMEWORK-4.
 FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11939 MW; E8011187E6F6FB9 CRC64;

Query Match 77.6%; Score 434; DB 1; Length 108;
 Best Local Similarity 79.4%; Pred. No. 1.2e-38;
 Matches 85; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGVITTCASQNVGTNVAWYQOKPGKAPKALISAFLYSGVPY 60
 DB 1 DIQMTQSPSSLSASVDGVITTCASQNVGTNVAWYQOKPGKAPKALISAFLYSGVPY 60
 QY 61 RFGSGSGTDFLTITISLPEDFATYYCOQYNIYPLTFGGGTVEIK 107
 DB 61 RFGSGSGTDFLTITISLPEDFATYYCOQYNIYPLTFGGGTVEIK 107

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RESULT 10
KV1L_HUMAN STANDARD; PRT; 108 AA.
ID KV1L_HUMAN
AC P01604;
DR 21-JUL-1986 (Rel. 01, Created)
DR 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region kue.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=79237924; PubMed=112021;
RA Eultz M., Kley H.-P., Zeltner H.-J.;
RT "The primary structure of the Bence-Jones protein kue. The amino acid
RL sequence of the variable part of a human L-chain of the kappa-type.";
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC PIR: A01870; K1HUKU.
DR HSSP: P01607; 1WTU.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 35 49 FRAMEWORK-2.
FT DOMAIN 4 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 5 57 88 FRAMEWORK-3.
FT DOMAIN 6 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 7 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90E4E98 CRC64;

Query Match 77.3%; Score 432; DB 1; Length 108;
Best Local Similarity 76.6%; Pred. No. 1.9e-38;
Matches 82; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

OY 1 DIQMTPSSLSASVGDRTITCKASQNGTNVAMVQKPGKAPKALIIYSASFLYSGVY 60
DB 1 DIQMTPSSLSASVGDRTITCKASQNGTNVAMVQKPGKAPKALIIYSASFLYSGVY 60
OY 61 RSSGSGSGDTFTLTSSLOPEPFATYYCOQYNNIPLTFGQTKVEIK 107
DB 61 RSSGSGSGDTFTLTSSLOPEPFATYYCOQYNNIPLTFGQTKVEIK 107

RESULT 11
KV1P_HUMAN STANDARD; PRT; 108 AA.
ID KV1P_HUMAN
AC P01608;
DR 21-JUL-1986 (Rel. 01, Created)
DR 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Roy.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68362076; PubMed=5595110;
RA Hilschmann N.;
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT Cum.)";
RL Hope-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).

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RN [2]
RP REVISIONS TO 39 AND 41.
RA Hilschmann N., Barnakol H.U., Hess M., Langer B., Ponstingl H.,
RA Steinmetz-Kayne M., Suter L., Watanabe S.;
RL (In) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press,
RL New York (1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC PIR: A01874; K1HUKY.
DR HSSP: P80362; 1WTU.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 35 49 FRAMEWORK-2.
FT DOMAIN 4 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 5 57 88 FRAMEWORK-3.
FT DOMAIN 6 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 7 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11782 MW; F5ACED5A313DF3A CRC64;

Query Match 76.7%; Score 429; DB 1; Length 108;
Best Local Similarity 77.6%; Pred. No. 3.8e-38;
Matches 83; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

OY 1 DIQMTPSSLSASVGDRTITCKASQNGTNVAMVQKPGKAPKALIIYSASFLYSGVY 60
DB 1 DIQMTPSSLSASVGDRTITCKASQNGTNVAMVQKPGKAPKALIIYSASFLYSGVY 60
OY 61 RSSGSGSGDTFTLTSSLOPEPFATYYCOQYNNIPLTFGQTKVEIK 107
DB 61 RSSGSGSGDTFTLTSSLOPEPFATYYCOQYNNIPLTFGQTKVEIK 107

RESULT 12
KV1S_HUMAN STANDARD; PRT; 108 AA.
ID KV1S_HUMAN
AC P01611;
DR 21-JUL-1986 (Rel. 01, Created)
DR 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Wes.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81092279; PubMed=6778806;
RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
RT "Preparative separation of the tryptic hydrolysate of a protein by
RT high-pressure liquid chromatography. The primary structure of a
RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
RT Wes).";
RL Hope-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC PIR: A01877; K1HUKS.
DR HSSP: P80362; 1WTU.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 24 34 COMPLEMENTARITY-DETERMINING-1.

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FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Query Match 76.4%; Score 427; DB 1; Length 108;
Best Local Similarity 78.5%; Pred. No. 6.2e-38;
Matches 84; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVSGRVITTCASQNVGTNVAWYQKRGKAPKALITYSASFYISGVPT 60
D 1 DIOMTQSPSSLSASVSGRVITTCASQNVGTNVAWYQKRGKAPKALITYSASFYISGVPT 60
DB 1 DIOMTQSPSSLSASVSGRVITTCASQNVGTNVAWYQKRGKAPKALITYSASFYISGVPT 60
QY 61 RFGSGSGTDFTLTISLOPEDFATYCCQYNYPLTFEGGTVEIK 107
D 61 RFGSGSGTDFTLTISLOPEDFATYCCQYNYPLTFEGGTVEIK 107
DB 61 RFGSGSGTDFTLTISLOPEDFATYCCQYNYPLTFEGGTVEIK 107

RESULT 13
KV10_HUMAN STANDARD; PRT; 108 AA.
AC P01609;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Scw.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP MEDLINE=75059271; PubMed=4435756;
RA Eulitz M., Hilschmann N.;
RT "The primary structure of a human immunoglobulin L-chain of
RT kappa-type (Bence-Jones protein Scw.); II: The chymotryptic peptides
RT and the complete amino acid sequence."
RL Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01875; KIHUSW.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11764 MW; 32CECDDDF9644414 CRC64;

Query Match 76.0%; Score 425; DB 1; Length 108;
Best Local Similarity 75.7%; Pred. No. 1e-37;
Matches 81; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVSGRVITTCASQNVGTNVAWYQKRGKAPKALITYSASFYISGVPT 60
D 1 DIOMTQSPSSLSASVSGRVITTCASQNVGTNVAWYQKRGKAPKALITYSASFYISGVPT 60
DB 1 DIOMTQSPSSLSASVSGRVITTCASQNVGTNVAWYQKRGKAPKALITYSASFYISGVPT 60
QY 61 RFGSGSGTDFTLTISLOPEDFATYCCQYNYPLTFEGGTVEIK 107
D 61 RFGSGSGTDFTLTISLOPEDFATYCCQYNYPLTFEGGTVEIK 107
DB 61 RFGSGSGTDFTLTISLOPEDFATYCCQYNYPLTFEGGTVEIK 107
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DB 61 RFGSGSGTDFTLTISLOPEDIGNTYCCQYDNVPITFGGTVEIK 107
RESULT 14
KV10_HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Rel.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type L-chain, subgroup I (Bence-Jones protein Rel.); Isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site."
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RP MEDLINE=7603968; PubMed=1182131;
RA Epp O., Latman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein REI refined at 2.0-A resolution."
RL Biochemistry 14:4943-4952(1975).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01873; KIHURE.
DR PDB; IREI; 17-FEB-84.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E118BCE2A CRC64;
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Search completed: April 2, 2003, 14:37:38
Job time : 25 secs

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Query Match          75.7%; Score 423; DB 1; Length 108;
Best Local Similarity 77.4%; Pred. No. 1.6e-37;
Matches 82; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTTCASQNVGTNAVYQOKPGKAPRALIYSASFLYSGVPY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 DIQMTQSPSSLSASVGDRVTTCASQNDIKRYLMNYQOTPGKAPRLIYEASNLQAGVPS 60

QY 61 RFSGSGSGTDFTLTISLTQPEDPATYFCQYNIYPLTFGGGTKVEI 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 RFSGSGSGTDFTLTISLTQPEDPATYFCQYQSLPYTFGGGTKLQI 106

RESULT 15
KV1W_HUMAN
ID KV1W_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-6501418; PubMed-6091049;
RA Klobbeck H.G.; Combratio G.; Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).

CC -----
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CC -----
DR EMBL: X00965; CAA25477.1; ALT_TERM.
DR PIR: A01883; K1HWK.
DR HSSP: P01607; REI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL
FT CHAIN 1 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match          75.7%; Score 423; DB 1; Length 129;
Best Local Similarity 78.5%; Pred. No. 2e-37;
Matches 84; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTTCASQNVGTNAVYQOKPGKAPRALIYSASFLYSGVPY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 23 DIQMTQSPSSLSASVGDRVTTCASQNSISNLYMNYQOKPGKAPRLIYAASSLQSGVTS 82

QY 61 RFSGSGSGTDFTLTISLTQPEDPATYFCQYNIYPLTFGGGTKVEI 107
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 83 RFSGSGSGTDFTLTISLTQPEDSATYFCQYQSLPYTFGGGTKLEIK 129
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GenCore version 5.1.4.P5_4578
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OM protein - protein search, using sw model

Run on: April 2, 2003, 14:33:54 ; Search time 86 Seconds
(without alignments)
256.361 Million cell updates/sec

Title: US-09-875-221b-9

Perfect score: 559

Sequence: 1 DIQMTQSPSSLSASVGRVTR.....CQGYNIYPLTFGGCTKVEIK 107

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP rivirus:*
16: SP bacteriap:*
17: SP archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	451	80.7	108	4 Q9UL70	Q9UL70 homo sapien
2	448	80.1	108	11 Q8V1J0	Q8V1J0 mus musculu
3	438.5	78.4	107	4 Q96SA9	Q96SA9 homo sapien
4	436	78.0	108	4 Q9UL77	Q9UL77 homo sapien
5	427	76.4	108	4 Q9UL79	Q9UL79 homo sapien
6	416	74.4	116	4 Q96PF6	Q96PF6 homo sapien
7	415.5	74.3	107	4 Q9UL81	Q9UL81 homo sapien
8	394	70.5	108	4 Q9UL83	Q9UL83 homo sapien
9	387.5	69.3	109	4 Q9UL85	Q9UL85 homo sapien
10	385	68.9	214	11 Q9RIAS	Q9RIAS mus musculu
11	383	68.5	214	11 Q8R062	Q8R062 mus musculu
12	379	67.8	233	11 Q9LWS9	Q9LWS9 mus musculu
13	376	67.3	234	11 Q8VCP0	Q8VCP0 mus musculu
14	374.5	67.0	109	4 Q9UL78	Q9UL78 homo sapien
15	373	66.7	109	11 Q920E6	Q920E6 mus musculu
16	369	66.0	234	11 Q9LWF8	Q9LWF8 mus musculu

17	369	66.0	298	11 Q9GYF0	Q9GYF0 mus musculu
18	367	65.7	107	11 Q9JL84	Q9JL84 mus musculu
19	357	63.9	127	11 Q925S9	Q925S9 mus musculu
20	348.5	62.3	109	4 Q9UL86	Q9UL86 homo sapien
21	344	61.5	111	11 Q920E9	Q920E9 mus musculu
22	338	60.5	99	11 Q9JL74	Q9JL74 mus musculu
23	337.5	60.4	106	5 Q9UL10	Q9UL10 schistosoma
24	334.5	59.8	241	11 Q921A6	Q921A6 mus musculu
25	332.5	59.5	134	11 Q8VDD0	Q8VDD0 mus musculu
26	329	58.9	107	11 Q9ER29	Q9ER29 mus musculu
27	320.5	57.3	238	11 Q99M37	Q99M37 mus musculu
28	318.5	57.0	235	11 Q9JLW2	Q9JLW2 mus musculu
29	313.5	56.1	238	11 Q8VCI6	Q8VCI6 mus musculu
30	304.5	54.5	239	11 Q8VC55	Q8VC55 mus musculu
31	301	53.8	101	11 Q9JL78	Q9JL78 mus musculu
32	300	53.7	97	11 Q9JL76	Q9JL76 mus musculu
33	300	53.7	103	11 Q9JL80	Q9JL80 mus musculu
34	297.5	53.2	239	4 Q8TCD0	Q8TCD0 homo sapien
35	289	51.7	109	6 Q9N0M5	Q9N0M5 oryctolagus
36	289	51.7	114	4 Q9UL80	Q9UL80 homo sapien
37	289	51.7	234	11 Q8R028	Q8R028 mus musculu
38	287.5	51.4	104	11 Q9JL82	Q9JL82 mus musculu
39	248.5	44.5	237	4 Q8WT06	Q8WT06 homo sapien
40	242.5	43.4	237	4 Q8WUK4	Q8WUK4 homo sapien
41	234.5	41.9	236	4 Q96E61	Q96E61 homo sapien
42	231.5	41.4	110	4 Q8TE63	Q8TE63 homo sapien
43	221.5	39.6	108	4 Q96S80	Q96S80 homo sapien
44	219.5	39.3	233	4 Q8TBC9	Q8TBC9 homo sapien
45	217.5	38.9	112	4 Q96JDL	Q96JDL homo sapien

ALIGNMENTS

RESULT 1

ID Q9UL70 PRELIMINARY: PRT; 108 AA.
AC Q9UL70:
DT 01-MAY-2000 (TREMBLrel. 13 Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035044; AAD56280.1; -
DR HSSP: P01607; IPR1.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IGv; 1.
FT NON_TER 1
FT NON_TER 108
SO SEQUENCE 108 AA; 11633 MW; 87BEDC3E41FCCA37 CRC64;

Query Match 80.7%; Score 451; DB 4; Length 108;
Best Local Similarity 81.3%; Pred. No. 5.3e-40;
Matches 87; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Oy 1 DIQMTQSPSSLSASVGRVTRITCKASQNYGVNVAHQKPKAPKALYSASFLYSQVY 60
Db 1 DIQMTQSPSSLSASVGRVTRITCKASQNYGVNVAHQKPKAPKALYSASFLYSQVY 60

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DR Pfam; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B57F16 CRC64;

Query Match
Best Local Similarity 82.2%; Score 438.5; DB 4; Length 107;
Matches 88; Conservative 7; Mismatches 11; Indels 1; Gaps 1;

QY 1 DIOMTQSPTSLASVAGDVTITCKASQNWGNVMAYOQKPKRARKALITYSFLYSVPY 60
Db 1 DIOMTQSPTSLASVAGDVTITCKRSQSISSLYMWYOQKPKRARKALLIYAASSLQSGVPS 60

QY 61 RFGSGSGTDFTLTITSSLQPEDPATTYYCOQYNIXPLTFGGCTKYEIK 107
Db 61 RFGSGSGTDFTLTITSSLQPEDPATTYYCOQ-SYSTLPFGGCTKYEIK 106

RESULT 4
Q9UL77 PRELIMINARY; PRT; 108 AA.
Q9UL77;
AC Q9UL77;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RT [1].
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HMLB; AF035037; AAD56273.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match
Best Local Similarity 80.4%; Score 436; DB 4; Length 108;
Matches 86; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIOMTQSPTSLASVAGDVTITCKASQNWGNVMAYOQKPKRARKALITYSFLYSVPY 60
Db 1 DIOMTQSPTSLASVAGDVTITCKRSQSISSLYMWYOQKPKRARNLLIYAASSLQSGVPS 60

QY 61 RFGSGSGTDFTLTITSSLQPEDPATTYYCOQYNIXPLTFGGCTKYEIK 107
Db 61 RFGSGSGTDFTLTITSSLQPEDPATTYYCOQSYSTSWIFEGCTKYEIK 107

RESULT 5
Q9UL79 PRELIMINARY; PRT; 108 AA.
Q9UL79;
AC Q9UL79;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match
Best Local Similarity 70.5%; Score 394; DB 4; Length 108;
Matches 73; Conservative 17; Mismatches 17; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDRTYITCKASQNGTVNAMYQOKPGKAPKALITYSASFYSGVPY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSYSSNLAMYQOKPGQAPRLITYCATSRATGIRA 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 RSSGSGGTDFLTITSSLOPEDPATYCCQVNIYPLTFGQGTKEIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 RSSGSGGTDFLTITSSLOPEDFAVYCCQVNIYPLTFGPGTKVDIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
Q90L85 PRELIMINARY; PRT; 109 AA.
AC Q90L85;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Betney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035029; AAD56265.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
FT NON_TER 1 109
FT SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match
Best Local Similarity 69.3%; Score 387.5; DB 4; Length 109;
Matches 74; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 DIQMTQSPSSLSASVDRTYITCKASQNGTVNAMYQOKPGKAPKALITYSASFYSGVPY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EIVMTQSPATLSVSPGERATLSCMASQSYSSNLAMYQOKPGQAPRLITYCATSRATGIRA 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 RSSGSGGTDFLTITSSLOPEDPATYCCQVNIYPLTFGQGTKEIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 RSSGSGGTDFLTITSSLOPEDFAIYCCQVNIYPLTFGGGTKEIK 108
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
Q9RIAS PRELIMINARY; PRT; 214 AA.
AC Q9RIAS;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Kappa light chain of Mab7 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.R.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
   antibody (Mab 7, its light and heavy chains) and construction of a
   RT single chain antibody (scFv).";
RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152371; AAD40242.1; -.
DR HSSP; P01679; 2PBJ.
DR InterPro; IPR003600; IG_Like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IgV_1.
DR SMART; SM00410; IG_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1 214
FT SEQUENCE 214 AA; 23922 MW; 52BA205FDE95E2A CRC64;

Query Match
Best Local Similarity 68.9%; Score 385; DB 11; Length 214;
Matches 71; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDRTYITCKASQNGTVNAMYQOKPGKAPKALITYSASFYSGVPY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 DIQMTQSPSSMASLGERVTITCKASQDINSYLSWFOQKPGKSPKTLIRANRLVDGVS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 RSSGSGGTDFLTITSSLOPEDPATYCCQVNIYPLTFGQGTKEIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 RSSGSGGTDFLTITSSLEEDMGITYCIQYDEFPRTFGSGTKLEIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
Q8R062 PRELIMINARY; PRT; 234 AA.
AC Q8R062;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-COLON;
RA Strausberg R.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027418; AAH27418.1; -.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEB1 CRC64;

Query Match
Best Local Similarity 68.5%; Score 383; DB 11; Length 234;
Matches 73; Conservative 13; Mismatches 21; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDRTYITCKASQNGTVNAMYQOKPGKAPKALITYSASFYSGVPY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 21 DIQMTQSSLSASLGDRTYITCKASQGISNLYNMYQOKPGDGTAKLITYTSSLSGVPS 80
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 RSSGSGGTDFLTITSSLOPEDPATYCCQVNIYPLTFGQGTKEIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 81 RSSGSGGTDFLTITSSLEPEDIAIYCCQVNIYPLTFGSGTKLEIK 127
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
Q9IWS9 PRELIMINARY; PRT; 233 AA.
AC Q9IWS9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

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	Matches	71;	Conservative	15;	Mismatches	21;	Indels	0;	Gaps	0;
Qy	1	DIQMTQSPSSLSASVGDRVTITCKASQNVGTNAVYQQRKAPKALITYSASFLYSGVPY	60							
Db	1	DIQMTQSPASLSASVGETVITTCRASGNHNYLAWYQQRKSPOLLVYNAKTLADGVPS	60							
Qy	61	RFGSGSGTDFLTISLQPEDFATYYCOQXNYPLTFGGTKVEIK	107							
Db	61	RFGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPMTFGGTRKLEIK	107							

Search completed: April 2, 2003, 14:39:10
 Job time : 87 secs